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GenCore version 5.1.6
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Copyright (c) 1993 - 2004 Compugen Ltd.	ng sw model	June 8, 2004, 12:30:12 ; Search time 0.001 Seconds (without alignments)
right (c) 1993 -	OM nucleic - nucleic search, using sw model	3, 2004, 12:30:12
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	OM nucl	Run on:
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63.400 Million cell updates/sec US-10-003-919-21 20 1 ATGGACTCGCTGGCACGCAC 20

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

264 Total number of hits satisfying chosen parameters: 132 seqs, 1585 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 132 summaries

rnpdb:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		tion	ce 21, Appl	48,	28,	28,	7618	7619,	7618,	7619,	619, 7	9914,	9915,		156	99	928		23	28	28	14	47	47	74	18	ດັ	5	10	10	30	41,	41,	ce 34, Appl	e 34
		Description	Seguence		Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sednence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequen	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguenc	Seguenc
SUMMARIES		QI	US-10-003-919-21	-10-712-672-4	-09-790-264-2	10-269	138	10-138-674-7619	7-949A-76	10-287-949A-761	2	19-866-108-991	9-86	10-71	10-712-672-15	10-312-273-661	9-848	1-160-388-9	1-435-696)-138-674-58	-949	9-825-805-14	9-740-332-47	9-817-879-47	-10-339-674-74	-10-339-674-18	-10-096-718-9	-10-096-718-29	-10-347-510A-1	-09-544-934B-10	-10-189-956-30	-10-138-674-414	10-287-949A	-10-291-230-	US-10-291-249-34
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		Score	20	12.2	11.8	11.8	11.4	11.4	11.4	11.4	11.4	11.2	11.2	11.2	10.8	10.4	10.4	10.4	10.4	10.4	10.4	10.2	10.2	10.2	10.2	10.2	10	10	10	10	ω. Θ	9.	9.0	9.4	9.4
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Sequence 3847, Ap Sequence 1313, App Sequence 1189, Ap Sequence 1189, Ap Sequence 1189, Ap Sequence 1189, App Sequence 51, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 12, Appl Sequence 13, Appl Sequence 15, Appl Sequence 16, Appl Sequence 22, Appl Sequence 2	equence 56 equence 1, equence 56 equence 10 equence 13
US-10-084-839-3847 US-10-033-145-833 US-10-033-145-833 US-10-330-627-1189 US-09-238-351-45 US-09-238-351-47 US-09-238-351-53 US-09-238-351-53 US-09-238-351-53 US-09-245-105A-59 US-09-245-105A-59 US-09-245-105A-59 US-09-245-105A-59 US-09-245-105A-59 US-09-245-105A-59 US-09-245-105A-59 US-09-245-105A-59 US-09-245-105A-61 US-09-39-146-128 US-10-011-670-79 US-10-011-670-79 US-10-011-670-79 US-10-011-670-79 US-09-989-789-2216 US-09-989-789-2216 US-09-989-789-2216 US-09-989-789-2216 US-09-989-789-2216 US-09-989-789-2216 US-09-989-789-2286 US-09-989-789-286 US-09-989-789-286 US-09-989-789-105-86 US-09-989-789-105-88	US-09-990-186-56 US-09-916-443A-1 US-09-918-994-56 US-09-989-994-56 US-10-257-021-10 US-10-033-145-13
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0 000000000000 000 0 00 0 0 0 0 0 0 0	

DB 1,

rnp

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ch 61.0%; Score 12.2; D
1 Similarity 64.7%; Pred. No. 9;
11; Conservative 3; Mismatches
PRIOR APPLICATION NUMBER: ..., ..., ..., PRIOR FILING DATE: 2000-08-31
FRICK PEDLICATION NUMBER: 60/197, 769
FRICK PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/150, 713
PRIOR APPLICATION NUMBER: 60/150, 713
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEG ID NOS: 5586
SOFTWARE: Patentin version 3.0
SEQ ID NO 48
LENGTH: 17
TYPE: RNA
TYPE: RNA
         APPLICATION NUMBER: US/09/653,225
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US-10-269-353-28/c
; Sequence 28, Application US/10269353
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                                                                                                                                                                                                                                                                                                                                                                                                                      2 TGGACTCGCTGGCACGC 18
                                                                                                                                                                                                                                                           CRGANISM: Homo sapiens
US-10-712-672-48
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Best Local Similarity
Matches 11; Conservat
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US-09-790-264-28/c
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Sequence 48, Application US/10712672
Sequence 48, Application US/10712672
Sequence 48, Application US/20040102413A1
SENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blarat
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
TITLE OF INVENTION: WORDER: US/10/112,672
CURRENT APPLICATION NUMBER: US/10/712,672
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              Sequence 475, App
Sequence 546, App
Sequence 567, App
Sequence 1224, App
Sequence 1224, App
Sequence 656, App
Sequence 1122, App
Sequence 1122, App
Sequence 1226, App
Sequence 126, App
Sequence 97, App
Sequence 98, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 177, App
Sequence 177, App
Sequence 177, Appl
Sequence 177, Appl
Sequence 177, Appl
Sequence 177, Appl
Sequence 175,03,
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Sequence 17
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Sequence 21, Application No. US20030114401A1
GENERAL IRPORANTION:
GENERAL IRPORANTION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
ITTLE REFERENCE: RTS-025E
FILE REFERENCE: RTS-025E
CURRENT APPLICATION NUMBER: US/10/003,919
CURRENT PILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 87
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 0.21;
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            US-10-033-145-475

US-10-033-145-479

US-10-033-145-567

US-10-033-145-567

US-10-033-145-567

US-10-330-627-563

US-10-330-627-693

US-10-330-627-1227

US-10-330-627-1327

US-10-330-627-1328

US-10-330-627-1328

US-10-330-627-1328

US-10-330-627-1328

US-10-330-627-1328

US-10-137-019-98

US-10-137-019-98

US-10-137-019-98

US-10-137-019-98

US-10-137-018-1368

US-10-137-018-1368

US-10-137-018-1368

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US-10-137-018-1368

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US-10-137-018-137-1368

US-10-027-632-175703

US-10-027-632-175703

US-10-027-632-175703

US-10-027-632-175703

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US-10-027-632-175703

US-10-027-632-175703
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-919-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 20; Conservative
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Sequence 28, Application US/09790264
| Sequence 28, Application US/09790264
| Patent No. US20020286081
| GENERAL INFORMATION
| APPLICANT: Holtzman, Douglas A. APPLICANT: Goodearl, Andrew D.J.
| APPLICANT: Holtzman, Douglas A. APPLICANT: Holtzman, Douglas A. APPLICANT: Holtzman, Douglas A. APPLICANT: Holtzman, Douglas A. APPLICANT: MCGARLY, Sean A. TITLE OF INVENTION: WEGGRASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, TITLE OF INVENTION: USES
| TITLE OF INVENTION: USES: 1200-02-21
| PRIOR APPLICATION NUMBER: US 09/065,661
| PRIOR APPLICATION NUMBER: US 09/289,531
| PRIOR APPLICATION NUMBER: US 09/280,531
| PRIOR FILING DATE: 1998-04-23
| PRIOR FILING DATE: 1998-04-23
| PRIOR FILING DATE: 1998-06-22
| PRIOR FILING DATE: 1998-07-29
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86.7%; Pred. No. 11;
tive 0; Mismatches
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TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 86.7
Matches 13; Conservative
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US-10-136-674-7619/C

US-10-136-674-7619/C

Sequence 7619, Application US/10138674

Fublication No. US20040077565A1

GENERAL INPORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Rocobedo, Jame

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MEHBOO-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 2002-05

SOFTWARE: Patentin version 3.0

SET OF TOWN TO 7519

LENGTH 177
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Sequence 7618, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bavoo, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: McSwiggen, Jim

APPLICANT: Bavoobe, Jaime

TITLE OF INVENTION: Mcthod and Reagent for the Treatment of Diseases or Conditions Rel

TITLE OF INVENTION: Mcthod and Reagent for the Treatment of Diseases or Conditions Rel

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TITLE OF INVENTION: Mcthod and Reagent for the Treatment of Diseases or Conditions Rel

TITLE OF INVENTION: Mcthod and Reagent for the Treatmen
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Best Local Similarity 92.3%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 1; Indels
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Pred. No. 13;
0; Mismatches
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US-10-287-949A-7619/c
i Sequence 7619, Application US/10287949A
; Publication No. US20040102389A1
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Best Local Similarity 92.3
Matches 12; Conservative
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2 TGGACTCGCTGGC 14
                                                   TGTACTCGCTGGC 5
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US-10-138-674-7619
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US-10-287-949A-7618
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; Sequence 768, Application US/20138674
; Publication No. US2044007565A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: Barobedo, Jam
    APPLICANT: Stinchcomb, Dan
    APPLICANT: Stinchcomb, Dan
    APPLICANT: Becobedo, Jaime
    APPLICANT: Becobedo, Jaime
    APPLICANT: Becobedo, Jaime
    APPLICANT: APPLICANTON: Method and Reagent for the Treatment of Diseases or Conditions Re
    TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
    TITLE OF INVENTION: Marbor of Vascular Endothelial Growth Factor Receptor
    CURRENT APPLICANTON NUMBER: US/10/138,674
    CURRENT FILING DATE: 2002-05-03
    NUMBER OF SEQ ID NOS: 20822
    SOFTWARE: PatentIn version 3.0
    SEQ ID NO 718
    LENGTH: 17
                         GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: MCGARTHY. Sean A.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
TITLE APPLICATION NOWHER: US/10/269,353
CURRENT APPLICATION NUMBER: US 09/790,264
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1999-06-22
PRIOR PLING DATE: 1999-06-22
PRIOR PLING DATE: 1999-06-22
PRIOR PLING DATE: 1999-07-29
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US-10-269-353-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
        Publication No. US20030104447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TGGACTCGCTGGCAC 16
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CRGANISM: Homo sapiens
US-10-138-674-7618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-10-138-674-7618/c
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| GENERAL INFORMATION:
| APPLICANT: GU, Yizhong
| APPLICANT: GU, Yizhong
| APPLICANT: GU, Yizhong
| APPLICANT: GU, Yizhong
| APPLICANT: FENN: Barron G.
| APPLICANT: FANK, David R.
| APPLICANT: RANK, David R.
| APPLICANT: SHANNOW, Mark
| TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
| TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
| CURRENT APPLICATION NUMBER: US/09/866,108
| CURRENT FILING DATE: 2001-05-25
| CURRENT FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2000-05-26
| PRIOR PLICATION NUMBER: GB 24263.6
                              APPLICANT: CHEN, MAYOLA N.
APPLICANT: CHEN, MAINTHAN MENABHORM
TITLE OF INTENTION: WATCH
TITLE OF INTENTION: WATCH
TITLE OF INTENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT PALLICATION NUMBER: US/09/866,108
CURRENT PALLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR
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0; Mismatches
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81.2%; Pred. No. 15
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Best Local Similarity 81.2'
Matches 13, Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-9914
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Bavco, Pam
APPLICANT: General Services of the Pharmaceuticals, Inc.
APPLICANT: Stinchcomb, Dam
APPLICANT: Stinchcomb, Dam
APPLICANT: Stinchcomb, Dam
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: MANBER: US/10/287, 949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SEQ ID NOS: 20822
SEQ ID NO 7619
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 619, Application US/10712672
; Sequence 619, Application US20040102413A1
; Sequence 619, Application No. US20040102413A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: Chowriza, Bharat
    APPLICANT: Chowriza, Bharat
    APPLICANT: Abswiggen, Jim
    APPLICANT: Abswiggen, Jim
    APPLICANT: McSwiggen, Jim
    APPLICANT: McMan and Reagent for the Inhibition of Telomerase Enzyme
    TILE REFERENCE: MBHB00-882-C (400/019)
    CURRENT APPLICATION NUMBER: US/09/653,225
    PRIOR FILING DATE: 2000-08-31
    PRIOR FILING DATE: 2000-08-31
    PRIOR FILING DATE: 2000-04-14
    PRIOR FILING DATE: 1999-08-31
    NWHBER OF SEQ ID NOS: 5586
    SOFTHARE: PatentIn Version 3.0
    SEQ ID NO 619
    LENGTH: 17
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Pred. No. 13;
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Pred. No. 13;
2; Mismatches
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0; Mismatches
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Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: GI, Yonggang
APPLICANT: PENN, Sharron G,
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.0%;
76.9%;
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92.3%;
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Best Local Similarity 76.9
Matches 10; Conservative
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Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7619
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US-10-712-672-619
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US-09-866-108-9914/c
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US-10-712-672-619
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Sequence 1569, Application US/10712672

Sequence 1569, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Biologue, Jim
APPLICANT: Stinchomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
TITLE OF INVENTION: Method and Reagent for 2003-11-13
FILE REFERENCE: MBH500-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT PILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: 60/150,713

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SOFUTH NO 1560
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       Indels
       3;
   Mismatches
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                                                                       2 TGGACTCGCTGGCACG 17
                                                                                                                  2 UGCGCUCUCUGGCACG 17
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Best Local Similarity 71.4%;
Matches 10; Conservative
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       10; Conservative
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ORGANISM: Homo sapiens
US-10-712-672-1569
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US-10-712-672-1569
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LENGTH: 16
       Matches
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Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jun
APPLICANT: McSwiggen, Jun
APPLICANT: McSwiggen, Jun
APPLICANT: ALICANCE McHod and Reagent for the Inhibition of Telomerase Enzyme
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
TITLE OF INVENTION WWHER: US/00/19)
CURRENT APPLICATION WUMBER: US/09/653,225
CURRENT PILING DATE: 2000-08-31
PRIOR APPLICATION WUMBER: 60/197,769
PRIOR APPLICATION WUMBER: 60/197,769
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SSCYTWARE: Patentin version 3.0
LENGTH: 17
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Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches
                            PRIOR FILLING DATE: 2000-10-30
PRIOR FILLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SEQ ID NOS: 15752
SEQ ID NO 9915
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108-9915
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COGANISM: Homo sapiens
US-10-712-672-618
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Best Local Similarity
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Sequence 232, Application US/10435696

| Sequence 232, Application US/10435696
| Publication No. US20040018525A1
| GENERAL INFORMATION:
| APPLICANT: Watez, Ralph
| APPLICANT: Watez, Ralph
| APPLICANT: Watez, Ralph
| APPLICANT: Munes, Marc
| TITLE OF INVENTION: METEVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
| FILE REFERENCE: LeA 36 108
| CURRENT FILING DATE: 2003-02-03
| PRIOR APPLICATION NUMBER: EP02010291.9
| PRIOR APPLICATION NUMBER: EP02010291.9
| PRIOR FILING DATE: 2002-05-21
| NUMBER OF SEQ ID NOS: 314
| SEQ ID NO 232
| LEMETH: 16
| LEMETH: LEMETH: 16
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Sequence 5820, Application US/10138674

Sequence 5820, Application No. US20040077565A1

SEQUENCE TO SECOND NO. US20040077565A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: Baccobedo, Jam

APPLICANT: Baccobedo, Jam

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Baccobedo, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION UNMBER: US/10/138,674

CURRENT FILING DATE: 2002-6.03

NUMBER OF SEQ ID NOS: 20822

SEQ ID NO 5820

SEQ ID NO 5820

LENGTH: 16
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Pred. No. 20;
0; Mismatches
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0; Mismatches
    Mismatches
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COTHER INFORMATION: D17S946 reverse primer US-10-435-696-232
       1;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                               3 GGACTCGCTGGCAC 16
                                                                            14 GGTCTCSCTGTCAC 1
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         11; Conservative
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CRGANISM: Homo sapiens
US-10-138-674-5820
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                RESULT 17
US-10-435-696-232/c
         Matches
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Publication No. US20030073207A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Braymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
FILE REFERENCE: MRHEDO-958-1 (400/018)
CURRENT APPLICATION NUMBER: US/09/848,754A
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEC ID NOS: 9645
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9285
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-9285
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Pred. No. 19;
0; Mismatches 1; Indels
                                                                                                                                             DB 1; Length 12;
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PUBLICATION NO. US20040072161A1

GENERAL INFORMATION:

APPLICANT: Genaiseance Pharmaceuticals, Inc.

APPLICANT: Bieglecki, Karyn

APPLICANT: Bieglecki, Karyn

APPLICANT: Sanchis, Angela

APPLICANT: Sanchis, Angela

APPLICANT: Sanchis, Angela

APPLICANT: Sanchis, Naha

TITLE OF INVENTION: HAPLOTYPES OF THE F2RL1 GENE

FILE REPRENCE: F2RL1 WWH-1785US

CURRENT APPLICATION NÜMBER: US/10/160,388

CURRENT FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-10

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PARCHING DATE: 2000-11-10

SEQ ID NO 9

LENGTH: 15
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Pred. No. 19;
                                                                                                                                        ch 52.0%; Score 10.4; I Similarity 91.7%; Pred. No. 17; 11; Conservative 0; Mismatches
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78.6%;
                                                                     ; OTHER INFORMATION: Primer tail US-10-312-273-661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Artificial Sequence
         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conserva
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Best Local Similarity
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US-10-160-388-9/c
                                                                                                                                             Query Match
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Sequence 4783, Application US/09817879

Sequence 4783, Application US/09817879

Publication No. US20030171311A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Hepatitis C Virus Infection

TITLE OF INVENTION: 9109/817,879

CURRENT PILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9703

SEQ ID NO 4783

ILENGTH: 15
                                                                                                                                                                                                                                                                                                            RESULT 21

Sequence 4783, Application US/09740332

Sequence 4783, Application US/09740332

Publication No. US2003012527041

GENERAL INPORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relateration File References: Republication Number: US/09/740,332

CURRENT APPLICATION NUMBER: US/09/740,332

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9704

SOFTWARE: Patentin version 3.0
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                                      Indels
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ed. No. 21;
Mismatches
    66.7%; Pred. No.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                          16
                                                                                                                                                                    1 UGGAGCCGCUGACAC 15
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Best Local Similarity 66.7
Matches 10, Conservative
                                                                                                                      2 TGGACTCGCTGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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LENGTH: 15
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GEQUENCE 119. Application US/09825805

Publication No. US2030004122A1

GEDIAT: No. US2030004122A1

GEDIAT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Reigalman, Leo

APPLICANT: Beaudry, Amber

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Sweedler, Dave

APPLICANT: Sheedler, Dave

APPLICANT: Sweedler, Dave

APPLICANT: Sweedler, Dave

APPLICANT: Sweedler, Dave

APPLICANT: Sweedler, Dave

APPLICANT: NUMBER: 09/78,23

PRIOR FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: 09/476,387

PRIOR APPLICATION NUMBER: 09/476,387

PRIOR APPLICATION NUMBER: 09/414,32

PRIOR FILING DATE: 1999-04-29

PRIOR FILING DATE: 1999-04-29

PRIOR FILING DATE: 1999-11-04

PRIOR FILING DATE: 1999-04-29

PRIOR FILING DATE: 1999-11-05

NUMBER: 09/186,675

PRIOR FILING DATE: 1999-04-29

PRIOR FILING DATE: 1998-04-29

PRIO
                                                                                                                                           Sequence 5820, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION
TO US20040102389A1
GENERAL INFORMATION
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TO EACH TO US EACH TO 
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Pred. No. 20;
0; Mismatches
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Best Local Similarity 91.7%;
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-10-287-949A-5820
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CORGANISM: Homo sapiens
US-09-825-805-143
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US-09-825-805-143
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Tita Anderson Hollerup
TITLE OF INVENTION: No. US20040063110Alel Process For The Detection of Mycobacte
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESSE: FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER
STREET: 1300 I ST. NW
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US-10-096-718-29/C
US-10-096-718-29/C
Sequence 29, Application US/10096718
Publication No. US20030032029A1
GENERAL INFORMATION:
APPLICANT. COllina, Mark
TITLE OF INVENTION: INTEGRATION
TITLE OF INVENTION: INTEGRATION
TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
FILE REFERENCE: 236/039
CURRENT APPLICATION NUMBER: US/10/096,718
FRICH APPLICATION NUMBER: US/10/096,718
FRICH PALLOR OF SEQ ID NOS: 79
SEQ ID NO 29
LENGTH: 12
LENGTH: 12
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                                                                                                                                                                                      DB 1; Length 12; 20;
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APPLICATION NUMBER: US/10/347,510A
FILING DATE: 21-Jan-2003
                                                                                                                                                                                    Query Match 50.0%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 20; Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTX...
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5 in
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCXI
COMPUTER: MICLOSOFT WORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: District of Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 105, Application US/10347510A
; Publication No. US20040063110A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Henrik Stender
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Microsoft Word
SEQ ID NO 9
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TGGCACGCAC 20
                                                                                                                                                                                                                                                                                                               2 TGGCACGCAC 11
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                                                                                                                                                                                                                                                                                      11 TGGCACGCAC
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CORGANISM: SYNTHETIC
US-10-096-718-29
                                                                                                ; TYPE: DNA; ORGANISM: SYNTHETIC
US-10-096-718-9
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2506
US-10-339-674-1891
                                                                                                                                                                                                                                                                                                                                                                                                        965
                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (744641)...(744657)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
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Publication No. US20030204318A1

GENERAL INFORMATION:

APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.

FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333

CURRENT PELING DATE: 2003-06-06

NUMBER OF SEQ ID NOS: 3537

SOFTWARE: Proprietary

SEQ ID NO 1891

LENGTH: 15
                   Sequence 740, Application US/10339674

Sequence 740, Application US/10339674

Publication No. US20030204318A1

GENERAL INFORMATION:

APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

TITLE OF INVENTION: Bacherichia coli K-12 MG1655 complete genome. TITLE OF INVENTION: Bacherichia coli K-12 MG1655 complete GUNRENT APPLICATION NUMBER: US/10/339,674

CURRENT FILING DATE: 2003-06-06

NUMBER OF SEQ ID NOS: 3537

SOFTWARE: Proprietary

SEQ ID NO 740

LENGTH: 15
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Publication No. US20030032029A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR TITLE OF INVENTION: INTEGRATING
TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
FILE REPERENCE: 236/039
CURRENT APPLICATION NUMBER: US/10/096,718
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 1998-12-21
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ORGANISM: Escherichia coli K-12 MG1655 complete genome.
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10.2; DB 1;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10.2; DB; Pred. No. 21; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Best Local Similarity 80.0%;
Matches 12; Conservative
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Best Local Similarity 80.0%;
Matches 12; Conservative (
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US-10-339-674-1891
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US-10-096-718-9
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CORRESSPONDERS: 123
CORRESSPONDERS: ADDRESSER: FINNEGAN, HENDERSON, FARABOW, GARRETT, & DUNNER STREET: 1300 I ST. NW
CITY: Mashington
STATE: District of Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/544,934B
FILING DATE: 07-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,392
FILING DATE: 15-0ct-96
APPLICATION NUMBER: 60/029,595
FILING DATE: 23-0ct-96
APPLICATION NUMBER: 60/045,962
FILING DATE: 3-0ct-97
APPLICATION NUMBER: 08/43,777
FILING DATE: 3-0ct-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5 inch
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: ASCXI
SOFTWARE: Microsoft Word
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/028,392
FILING DATE: 15-0ct-96
APPLICATION NUMBER: 60/029,595
FILING DATE: 23-0ct-96
APPLICATION NUMBER: 60/045,962
FILING DATE: 08-MAY-97
APPLICATION NUMBER: 08/943,777
FILING DATE: 3-0ct-97
ATTORNEY/AGENT INPORMATION:
NAME: Anthony C. Tridico
REGISTRATION NUMBER: 45,958
TELECOMMUNICATION NUMBER: 45,958
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 408-4173
TELEFHONE: (202) 408-4100
INFORMATION FOR SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-347-510A-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Anthony C. Tridico
REGISTRATION NUMBER: 45,958
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4173
TELEPRAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid basepairs STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 105, Application US/09544934B Publication No. US20020137035A1 GENERAL INFORMATION:
APPLICANT: Henrik Stender
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 15 basepairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CGCTGGCACG 17
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RESULT 30
US-10-138-674-4143
Sequence 4143, Application US/10138674
Sequence 4143, Application US/10138674
Shill cation No. US20040077565A1
GENERAL INFORMATION:
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Revocy Pam
APPLICANT: Becobedo, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Secobedo, Jaime
TILLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 2002-05-03
SOFTWARET PALENTIN Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mirel, Daniel B
APPLICANT: Erlich, Henry A
APPLICANT: Bugawan, Teodorica L
APPLICANT: Bugawan, Teodorica L
APPLICANT: Bugawan, Teodorica L
APPLICANT: No. US20300152951Alle, Janelle A
APPLICANT: Valdes, Ana M
TITLE OF INVENTION: 1L-4 RECEPTOR SEQUENCE VARIATION ASSOCIATED WITH TYPE 1
TITLE OF INVENTION: DIABETES
FILE REPERENCE: 1803-295-999
CURRENT APPLICATION NUMBER: US/10/189,956
CURRENT FILING DATE: 2002-07-17
SUFFRENT FILING DAIS: 2002-07-17
SUFFRENT FILING DAIS: 62
SOFTWARE: PATENTIN VERSION 3.1
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. OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-189-956-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.6%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                      50.0%; Score 10; DB 1; Length 15; 100.0%; Pred. No. 23; trive 0; Mismatches 0; Indels
                                                                                                                                             TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 105:
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 basepairs
TYPE: mucleic acid basepairs
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/10189956 Publication No. US20030152951A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GGACTCGCTGGCA 15
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Best Local Similarity 100.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                           8 CGCTGGCACG 17
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ORGANISM: Homo sapiens
                                                                                                                                                                                                      US-09-544-934B-105
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LENGTH: 15
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LENGTH: 15
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      Indels
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US-10-291-249-34

US-10-291-249-34

US-10-291-249-34

Publication No. US20030119041A1

GENERAL INFORMATION:
APPLICANT: Ruffner, Duane E.
APPLICANT: Pierce, Michael L.
APPLICANT: Chen, Zhidong

TITLE OF INVENTION: Directed Antisense Libraries
FILE REPRENCE: T6678.US. B

CURRENT PILING DATE: 2002-11-07

CURRENT PILING DATE: 2002-11-07

PRIOR FILING DATE: 1999-03-28

PRIOR FILING DATE: 1999-03-28

PRIOR FILING DATE: 1998-03-28

PRIOR FILING DATE: 1998-03-28

PRIOR FILING DATE: 1998-03-28

PRIOR FILING DATE: 1998-01-06

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PATENTIN VERSION 31

SEQ ID NO 34

LENGTH: 14
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      0; Mismatches
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Argue, Brad T.
Bartholomay, Christian T.
Chehak, Ludanne
Curtis, Michelle L.
Eis, Peggy S.
Hall, Jeff G.
Ip, Hon S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3847, Application US/10084839, Publication No. US20030186238A1, GENERAL INFORMATION:
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Lukowiak, Andrew A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neri, Bruce P.
Olson, Sarah M.
Olson, Sarah M.
Schaefer, James J.
Skrzypczynski, Zbigniew
Takova, Testska Y.
Thompson, Lisa C.
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Lymaicheva, Natalie E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-249-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaiser, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.9
Matches 10; Conservative
      10; Conservative
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                                                                    3 GGACTCGCTGG
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          Matches
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APPLICANT RACO, Pam
APPLICANT RACO, Pam
APPLICANT REACO, Pam
APPLICANT RESCOLATION DESCRIPTION DE
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                                                                          Query Match
Best Local Similarity 61.5%; Pred. No. 26;
Matches 8; Conservative 3; Mismatches 2; Indels
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US-10-291-230-34

| US-10-291-230-34
| Sequence 34, Application US/10291230
| Publication No. US20030108939A1
| GENERAL INPORMATION:
| APPLICANT: Ruffner, Duane B. APPLICANT: Pierce, Michael L. APPLICANT: Chen, Zahidong
| TITLE OF INVENTION: Directed Antisense Libraries FILE REFERENCE: T6678.US.A.
| CURRENT APPLICATION NUMBER: US/10/291,230
| CURRENT APPLICATION NUMBER: US 09/647,344
| PRIOR PILING DATE: 2000-12-04
| PRIOR PLING DATE: 1998-03-28
| PRIOR FILING DATE: 1998-03-28
| PRIOR FILING DATE: 1998-03-28
| PRIOR PLING DATE: 1998-13-28
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Best Local Similarity 61.5%; Pred. No. 26;
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4143, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
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; ORGANISM: herpes simplex virus
US-10-291-230-34
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1 AUGGAAUCUCUGG 13
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Best Local Similarity
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US-10-287-949A-4143
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                       US-10-138-674-4143
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LENGTH: 15
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; ORGANISM: Homo sapiens
US-10-033-145-1372
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US-10-033-145-833

US-10-033-145-833

Sequence 833, Application US/10033145

Publication No. U520020151515A1

GENERAL INFORMATION:

APPLICANT: GENERTS CORPORATION

APPLICANT: SHANKARA, SRINIVAS

TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

FILE REFERENCE: GA0201C

CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT APPLICATION NUMBER: DCT/US99/13800

PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR PILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 2137

SOFTWARE: PatentIn version 3.0

LENGTH: 10

LENGTH: 10

LENGTH: 10

LENGTH: 10
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Sequence 1372, Application US/10033145
Publication No. US2020151515A1
Sequence 1372, Application US/10033145
Publication No. US2020151515A1
APPLICANT: GENEYTME CORPORATION
APPLICANT: SHAWRAR, SRINIVAS
TILE REFERENCE GAO201C
CURRENT PILLOR DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US/10/033,145
CURRENT PILLOR DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR PILLOR DATE: 1999-06-18
SOFTWARE PATENTIN VERSION 3.0
SEQ ID NO 1372
LENGTH: 10
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Pred. No. 30;
0; Mismatches 1; Indels
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100.0%; Pred. No. 28;
tive 0; Mismatches
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: Patentin version 3.1
LENGTH: 14
                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Best Local Similarity 90.9%;
Matches 10; Conservative
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; OTHER INFORMATION: Synthetic
US-10-084-839-3847
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-033-145-833
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US-09-238-351-45/c
Sequence 45, Application US/09238351
Fatent No. US20020006643A1
Fatent No. USA04
Fatent No. USA04
Fatent No. USA04
Fatent No. USA04
Fatent Reling DATE: 1998-01-29
FATENTER APPLICATION NUMBER: 09/014,304
FATENTER APPLICATION NUMBER: 06/073,011
FATENTER APPLICATION NUMBER: 60/074,425
FATENTER PILING DATE: 1998-01-29
FATENTER FILING DATE: 1998-01-20
FATENTER FILING DATE: 1998-01-20
FATENTER FILING DATE: 1998-01-20
FATENTER FILING DATE: 1998-01-6
FATENTER FILING DATE: 1998-01-6
FATENTER FILING DATE: 1998-01-16
FATENTER FILING DATE: 1998
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        Length 10;
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Query Match
45.0%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                        RESULT 37
US-10-330-627-1189
i Sequence 1189, Application US/10330627
i Publication No. US20030175771A1
i GENERAL INPORMATION:
i APPLICANT: Velculescu, Victor E.
i APPLICANT: Vogelstein, Bert
i TITLE OF INVENTION: Human Transcriptomes
i FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT PILING DATE: 1999-11-24
i NUMBER OF SEQ ID NOS: 1564
i SEQ ID NO 1189
i LENGTH: 10
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-10-330-627-1189
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RESULT 41
US-09-238-351-53/c
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US-09-238-351-59/c
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Sequence 47 Application US/09238351

Patent No. US20202006643A1

GENERAL INFORMATION:
APPLICANT: Bamdad, Cyntha

ITILE OF INVENTION: Amplification of Nucleic Acids with Electronic

TITLE OF INVENTION: Detection of Nucleic Acids with Electronic

TITLE OF INVENTION: Detection of Nucleic Acids with Electronic

TITLE OF INVENTION: Detection of Nucleic Acids with Electronic

TITLE OF INVENTION: Detection OF Nucleic Acids with Electronic

TITLE OF INVENTION: Detection OF Nucleic Acids with Electronic

TITLE OF INVENTION UNBER: US/09/238,351

CURRENT APPLICATION NUMBER: 09/014,304

EARLIER FILING DATE: 1998-01-27

EARLIER APPLICATION NUMBER: 60/034,011

EARLIER APPLICATION NUMBER: 60/084,509

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 83

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 47

LENGTH: 13
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Fatent No. USCO020006643A1
GENERAL INFORMATION:
APPLICANT: Bayrem, Jon Faiz
APPLICANT: Bayrem, Jon Faiz
FILE PARTICON:
FILE PERENEUE:
FILE OF INVENTION:
FILE PERENEUE:
FILE OF INVENTION:
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FILE PERENEUE:
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FILE OF INVENTION:
FILE OF INVENTION WINBER:
FILE APPLICATION NUMBER:
FILE FILING DATE:
FARLIER FILING DATE:
FARLIER PELING DATE:
FILE APPLICATION NUMBER:
FOLO84, 425
FARLIER PELING DATE:
FARLIER APPLICATION NUMBER:
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FARLIER APPLICATION NUMBER:
FARLIER FILING DATE:
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                                                                           Length 13;
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
                                                  45.0%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                      Conservative
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                                         Query Match
Best Local Similarity
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US-09-238-351-51/c
US-09-238-351-45
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Patent No. US20020006643A1
GENERAL INFORMATION:
APPLICANT: RAYPAN
TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic TITLE OF INVENTION: Detection
FILE REFERENCE: A67643/RFT/RMS
FILE REFERENCE: A67643/RFT/RMS
CURRENT FILING DATE: 1999-01-27
CURRENT FILING DATE: 1999-01-27
                                                                                                     FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
VS-09-238-351-53
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                                                                                                                                                           Length 13;
                                                                                                                                                          Query Match
45.0%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
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45.0%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 13
                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 61, Application US/09238351

Fatent No. US20020006643A1

GENERAL INFORMATION:
APPLICANT: Rayyem, Jon Faiz
APPLICANT: Rayyem, Jon Faiz
APPLICANT: Bandad, Cynthia
TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
TITLE OF INVENTION: Detection Nucleic Nucleic Acids with Electronic
TITLE OF INVENTION: Detection of Nucleic Acids with Electronic
TITLE OF INVENTION: Detection OF Nucleic Acids with Electronic
TITLE OF INVENTION: Detection OF Nucleic Acids with Electronic
FILE REFERENCE: A67643/RFT/RMS
CURRENT APPLICATION NUMBER: US/09/238,351

CURRENT FILING DATE: 1998-01-29

EARLIER PELING DATE: 1998-01-29

EARLIER PELING DATE: 1998-05-06

EARLIER PELING DATE: 1998-05-06

EARLIER PELING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 83

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 61

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LENGTHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-238-351-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels
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45.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels
                           EARLIER FILING DATE: 1998-01.27
EARLIER PELING DATE: 1998-01.27
EARLIER PELING DATE: 1998-01.29
EARLIER FILING DATE: 1998-02-29
EARLIER PILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 60/084,425
EARLIER APPLICATION NUMBER: 60/084,509
EARLIER PILING DATE: 1998-05-06
EARLIER PILING DATE: 1998-05-16
NUMBER OF SEQ ID NOS: 83
SOFFWARE: PALENTIN VOYS: 83
SEQ ID NO 59
LENGTH: 13
APPLICATION NUMBER: 09/014,304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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RESULT 44 US-09-510-378-23/c ; Sequence 23, Application US/09510378

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GENERAL INFORMATION:
GENERAL INFORMATION:
Miyada (Charles Garrett
Hubbell, Earl A.
Che, Mark
Fodor, Stephen P.A.
Huang, Xiaohua C.
Lipshutz, Robert J.
Lobban, Peter E.
Mortis, Macdonald S.
Sheldon, Edward L.
Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATIOM SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

RAPHICATION NUBER: US/09/510,378

FILING DATE: 22-Feb-2000

CLASSIFICATION: <underweependate

CLASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 250
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STRET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRANONMENES: 37,505
REFERENCE/DOCKET NUMBER: 018547-004130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/544,381

FILING DATE: -CUNKNOW 08/510,521

FILING DATE: 02-AUG-1995

APPLICATION NUMBER: US 08/510,521

FILING DATE: 26-OCT-1994

APPLICATION NUMBER: US 08/284,064

FILING DATE: 26-OCT-1994

APPLICATION NUMBER: US 08/143,312

FILING DATE: 26-OCT-1993
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
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MOLECULE TYPE: DNA (oligonucleotide)

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-510-378-23
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TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 45
US-09-798-260-81/c
US-09-798-260-81, Application US/09798260
; Publication No. US20030165830A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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Gape

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US-09-245-105A-47/c
US-09-245-105A-47/c
Sequence 47, Application US/09245105A
Sequence 47, Application US/09245105A
Sequence 47, Application No. US20303087228A1
GENERAL INFORMATION:
APPLICANT: Bamdad, Cynthia
APPLICANT: Tu, Changjun
TILE OF INVENTION: Electronic Detection of Nucleic Acids Using Monolayers
FILE REFERENCE: A-67652/RFT/RMS
CURRENT FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR PLILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084,509
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 83
SOFUMARE: Datentin Ver. 2.0
SEQ ID NO 47
LENGTH: 13
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US-09-245-105A-51/C
Sequence 51, Application US/09245105A
Sequence 51, Application US/09245105A
GENERAL INFORMATION:
APPLICANT: Bamdad, Cynthia
APPLICANT: Bundad, Cynthia
APPLICANT: Tu, Canagiun
TILE OF INVENTION: Electronic Detection of Nucleic Acids Using Monolayers
TILE REFERENCE: A-67652/RFT/RMS
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/084,425
PRIOR APPLICATION NUMBER: 60/084,509
PRIOR APPLICATION NUMBER: 09/135,183
PRIOR FILING DATE: 1998-05-06
SEQ ID NOS: 83
SEQ ID NOS: 83
LENGTHAR: Patentin Ver. 2.0
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-245-105A-47
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                                                                                                                                                                                                                     0; Indels
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                              Query Match 45.0%; Score 9; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 34; Matches 9; Conservative 0; Mismatches 0; Indels
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f: Cronin, Maureen T.

The Miyada, Charles G.

MT: Miyada, Charles G.

ANT: Chee, Mark

Lichar: Dedor, Stephen P. A.

Lichar: Lipshutz, Robert J.

Lichar: Lipshutz, Robert J.

Lichar: Lipshutz, Robert J.

Lichar: Morris, McDonald S.

Lichar: Ling of Naray Solay C.

TLE OF INVENTION: BIOTRANSFORMATION GENES

UTREAP TAILCATION NUMBER: US 08/778, 794

RRIOR FILING DATE: 1993-10-10

RRIOR FILING DATE: 1993-10-10

RRIOR FILING DATE: 1994-00-26

PRIOR FILING DATE: 1994-00-26

PRIOR FILING DATE: 1994-00-26

PRIOR APPLICATION NUMBER: US 08/284, 064

RRIOR FILING DATE: 1994-00-26

PRIOR APPLICATION NUMBER: US 08/143, 312

PRIOR APPLICATION NUMBER: US 08/143, 312

PRIOR APPLICATION NUMBER: US 08/143, 312

PRIOR FILING DATE: 1994-00-26

WUMBER OF SEQ ID NOS: 156

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-245-105A-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45, Application US/09245105A
| Sequence 45, Application US/09245105A
| Publication No. US20030087228A1
| GENERAL INFORMATION:
| APPLICANT: Bandad, Cynthia
| APPLICANT: Wu, Changlun
| TITLE OF INVENTION: Electronic Detection of TITLE OF INVENTION: Blectronic Detection of TITLE OF INVENTION: Blectronic Detection of Nucrita Reperence: A-67652/RFT/RMS
| CURRENT APPLICATION NUMBER: US/09/245,105A
| CURRENT FILING DATE: 1998-05-06
| PRIOR PAPLICATION NUMBER: 60/084,509
| PRIOR PILING DATE: 1998-05-06
| PRIOR APPLICATION NUMBER: 60/084,509
| PRIOR APPLICATION NUMBER: 09/135,183
| PRIOR APPLICATION NUMBER: 09/135,183
| PRIOR PILING DATE: 1998-08-17
| NUMBER OF SEQ ID NOS: 83
| LENGTH 13
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Gaps

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, OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-245-105A-51
                                               Length 13;
                                                  DB 1;
                                                  Score 9;
                                                  45.0%;
                                                    Query Match
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US-09-751-561-18
Matches
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Sequence 59, Application US/09245105A

Sequence 59, Application US/09245105A

PUDIcation No. US20030087228A1

GENERAL INFORMATION:

APPLICANT: Bandad, Cynthia

APPLICANT: Bandad, Cynthia

APPLICANT: Buckeric Electronic Detection of Nucleic Acids Using Monolayers

FILE REFERENCE: A-67652/RFT/RMS

CURRENT PAPLICATION NUMBER: 60/084,425

PRIOR APPLICATION NUMBER: 60/084,425

PRIOR APPLICATION NUMBER: 60/084,509

PRIOR APPLICATION NUMBER: 60/084,509

PRIOR PRIJNG DATE: 1998-05-06

PRIOR PRIJNG DATE: 1998-05-06

PRIOR PRILNG DATE: 1998-08-17

NUMBER OF SEQ ID NOS: 83

SEQ ID NO S9

SEQ ID NO S9

LENGTH: 13

FURNAL APPLICATION VINCENTIAL APPLICATION NUMBER: 00/084,509

SEQ ID NO S9

LENGTH: 13
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                         Gaps
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US-09-245-105A-53
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OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-245-105A-59
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                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 13;
                                                                                                                                                                                 RESULT 49
US-09-245-105A-53/c
is Sequence 33, Application US/09245105A
is Publication No. US20030087228A1
igeneral information:
GENERAL INFORMATION:
APPLICANT: Bandad, Cynthia
APPLICANT: Wu, Changjun
TITLE OF INVENTION: Electronic Detection of Nuc;
FILE REFERENCE: A-67652/RFT/RMS
CURRENT APPLICATION NUMBER: US/09/245,105A
CURRENT APPLICATION NUMBER: 60/084,425
FRIOR APPLICATION NUMBER: 60/084,425
FRIOR FILING DATE: 1998-05-06
FRIOR FILING DATE: 1998-05-06
FRIOR APPLICATION NUMBER: 09/135,183
FRIOR APPLICATION NUMBER: 09/135,183
FRIOR APPLICATION NUMBER: 09/135,183
FRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 83
individual NUMBER: Patentin Ver: 2.0
is SEQ ID NO 53
individual Number: 2.0
individual Number: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                     1 ATGGACTCG 9
                                                                                                    10 ATGGACTCG 2
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Best Local Similarity
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Patent No. US2010007985A1
GENERAL INPORMATION:
APPLICANT: Schoberg, Jonathan
APPLICANT: Deem, Michael
APPLICANT: Deem, Michael
APPLICANT: Deem, Michael
APPLICANT: Method for the Determination and
ITILE OF INVENTION: Classification of DNA Sequences in a Sample Without
TITLE OF INVENTION: Classification of DNA Sequences in Sample Without
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CONTRY: USA
ZIP: 10036-2711
COMPUTER REAABLE FOR:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,561
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Gaps
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels
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Mismatches
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/547,214
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ORGANISM: Artificial Sequence
9; Conservative
                                                                                         1 ATGGACTCG 9
                                                                                                                                                                         10 ATGGACTCG 2
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US-09-751-561-20
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Patent No. US20010007985A1
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: Suppen, John
TITLE OF INVENTION: Glassification of DNA Sequences in a Sample Without
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Permie and Edmonds
STREET: 1155 Avenue of the Americas
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ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,561
APPLICATION NOMBER: US/US/22,501
FILING DATE:
RIGH APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION
APPLICATION WHRER: 08/57,214
FILING DATE:
ATTONEY/ABOUT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET UNDAER: 7934-015-999
TELECOMMUNICATION INFORMATION:
TELEFRANCE (212) 790-9090
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44.0%; Score 8.8; DB
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches
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44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred, No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels
Score 8.8; DB 1; Length 12;
Pred. No. 35;
0; Mismatches 2; Indels
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US-099-364-24
Sequence 24, Application US/09989364
Sequence 24, Application US/09989364
Publication No. US20030003463A1
GENERAL INFORMATION:
APPLICANT: Nothers, Jonathan M
APPLICANT: Natlur, Girish N
APPLICANT: Natlur, Girish N
APPLICANT: Natlur, Girish N
APPLICANT: Natlur, Girish N
PITLE OF INVENTION: Methods and Devices for Measuring
TITLE OF INVENTION: Differential Gene Expression
FILE REFERENCE: 7934-021
CURRENT FILING DATE: 2011-11-21
PRIOR APPLICATION NUMBER: 09/203,231
PRIOR APPLICATION NUMBER: 09/203,231
PRIOR APPLICATION NUMBER: 09/203,231
PRIOR APPLICATION NUMBER: 09/203,231
PRIOR PRING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 12
                                                                                                                                                                                      RESULT 54
US-09-364-22
IS-09-989-364.22
| Sequence 22, Application US/09989364
| Publication No. US20030003463A1
| GENERAL INPORMATION:
| APPLICANT: Nallur, Girish N
| APPLICANT: Nallur, Girish N
| TILLS OF INVENTION: Methods and Devices for Measuring
| TILLS OF INVENTION: Differential Gene Expression
| TILLS OF INVENTION NUMBER: US/09/989,364
| CURRENT FILLING DATE: 1998-12-02
| PRIOR PLING DATE: 1998-12-02
| NUMBER OF SEQ ID NOS: 88
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 22
| LENGTH: 12
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0; Mismatches
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Best Local Similarity 83.3%;
Matches 10; Conservative
     Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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; OTHER INFORMATION: Primer
US-09-989-364-24
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COTHER INFORMATION: Primer
US-09-989-364-22
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Fublication No. US20020151515A1
GENERAL INFORMATION:
APPLICANT: GENERAL SERINIVAR
APPLICANT: ROBERTS, BRUCE
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: DC1/US99/13800
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR APPLICATION NUMBER: PCT/US99/13800
SPINREST FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin Version 3.0
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US-10-033-145-1384

US-10-033-145-1384

Sequence 1384, Application US/10033145

Publication No. US20020151515A1

GENERAL INFORMATION:
APPLICANT: GENEYME CORPORATION
APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS

TITLE OF INVERTION:
FILE REFERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
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Pred. No. 38;
0; Mismatches 1; Indels
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Pred. No. 38;
0; Mismatches 1; Indels
42.0%;
90.0%;
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-10-033-145-17
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US-10-293-222-11
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                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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US-09-817-879-4616/c
US-09-817-879-4616/c
Sequence 4616, Application US/09817879
Publication No. US20030171311A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RIDEZYME Pharmaceuticals Inc.
TITLE OF INVENTION: Hepetitis C Virus Infection
TITLE OF INVENTION: Hepetitis C Virus Infection
FILE REFERENCE: MHB00-801-F
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 4616
                                                                                                                       US-01-740-332-4616/c
US-03-740-332-4616/c
Sequence 4616, Application US/09740332
Sequence 4616, Application US/09740332
Publication No. US20030125270A1
GENERAL INFORMATION:
TITLE DE INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE REPERENCE: RP1 400/003
CURRENT APPLICATION UNDER: US/09/740,332
CURRENT PILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: Patentin version 3.0
SEQ ID NO 4516
LENGTH: 13
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44.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION:
NOTHER INFORMATION: oligonuclectide substrate
US-09-740-332-4616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
COTHER INFORMATION: oligonucleotide substrate US-09-817-879-4616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 58
US-10-293-222-11/c
; Sequence 11, Application US/10293222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA ORGANISM: Artificial Sequence
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Publication No. US20040033932A1

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) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ) OTHER INFORMATION: Oligonucleotide US-10-005-212-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 38;
0; Mismatches 1; Indels
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US-10-330-627-406/C
Sequence 406, Application US/10330627
PUDLICATION NO. US20030175771A1
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor B.
APPLICANT: Vogelstein, Bert
TITLE NEFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SEQ ID NO 406
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                             42.0%; Score 8.4; DB 90.0%; Pred. No. 38; tive 0; Mismatches
                          CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin version 3.0
SEQ ID NO 1384
LENGTH: 10
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90.0%;
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ORGANISM: Artificial Sequence
FEATURE:
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CRGANISM: Homo sapiens
US-10-330-627-406
                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-10-033-145-1384
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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US-10-441-495-25/C

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US-10-441-495-25/C

US-10-441-495-25/C

US-10-441-495-25/C

Explication No. US-20040005613Atch, Michael

APPLICANT: No. US-20040005613Atch, Michael

APPLICANT: No. US-20040005613Atch, Michael

TITLE OF INVENTION: Methods, Probes, and Accessory Molecules for Detecting Single

TITLE OF INVENTION: Muchods, Probes, and Accessory Molecules for Detecting Single

TITLE OF INVENTION: Muchods, Probes, and Accessory Molecules for Detecting Single

TITLE OF INVENTION: Muchods, Probes, and Accessory Molecules for Detecting Single

TITLE OF INVENTION: Muchods, Probes, and Accessory Molecules for Detecting Single

TITLE OF INVENTION: Muchods, Probes, and Accessory Molecules for Detecting Single

FILE REFERENCE: MU-0010.P.1.1

CURRENT FILING DATE: 2003-05-20

PRIOR APPLICATION NUMBER: 60/387,831

PRIOR PILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.2

SEQ ID NO 25

LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: No. US20040005613Alton, Michael
APPLICANT: No. US20040005613Alton, Michael
TITLE OF INVENTION: Methods, Probes, and Accessory Molecules for Detecting Single
FILE OF INVENTION: Muclocide Polymorphisms
FILE OF INVENTION: Muclocide Polymorphisms
FILE SPERRENCE: MU-00101.P.1.1
CURRENT PILING DATE: US/10/441,495
CURRENT PILING DATE: 2003-05-20
PRIOR FILING DATE: 2002-05-22
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 26
SUFTWARE: PARENTING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 26
SUFTWARE: PARENTING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 26
SUFTWARE: PARENTING VERSION 3.2
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                                                            Gaps
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Score 8.4; DB 1; Length 11; Pred. No. 40;
                                                               0; Mismatches
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OTHER INFORMATION: synthetic construct
US-10-441-495-21
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                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/10441495 Publication No. US2004005613A1 GENERAL INFORMATION:
Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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ORGANISM: artificial sequence
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                                                                                                                           1 ATGGACTCGC 10
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US-10-441-495-21
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US-10-033-717-22/c
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Publication No. US20020039780A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Horvarth, Diana M.

APPLICANT: Chua, Nam-Hai

APPLICANT: Stuiver, Maarten H.

APPLICANT: Jensen Jan

FILE REFERENCE: P8/5-50067A

CURRENT FILING DATE: 1998-08-03

PRIOR FILING DATE: 1998-08-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15

LENGTH 10

TUDENCE IN 10

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; OTHER INFORMATION: Description of Artificial Sequence Primer AP1
US-09-777-207-15
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; Sequence 1287, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENERATION
; APPLICANT: SHORERS, BRUCE
; APPLICANT: SHORERS, BRINIVAS
; TITLE OF INVENTION: PEPRARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PATCHIL VERSION 3.0
; SEQ ID NOS: 2137
; SOFTWARE: PATCHIL VERSION 3.0
; SEQ ID NOS: 2137
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                                        Indels
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100.0%; Pred. No. 45;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 45;
tive 0; Mismatches
Best Local Similarity 90.0%; Pred. No. 40; Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                10 CTGGCACGCA 19
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US-10-033-145-1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TCGCTGGC 14
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US-10-033-145-1287/c
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US-09-777-207-15/c
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RESULT 68
US-10-079-954-3/C
| US-110-079-954-3/C
| Sequence 3, Application US/10079954
| Publication No. US20020168661A1
| Publication No. US20020168661A1
| GENERAL INFORMATION:
| APPLICANT: Durst, Matthias
| APPLICANT: Nees, Matthias
| APPLICANT: Nees, Matthias
| APPLICANT: Nees, Matthias
| PILE REFERENCE: SCHU 204 (09902857)
| PILE REFERENCE: SCHU 204 (09902857)
| CURRENT FILING DATE: 2002-02-19
| PRIOR FLING DATE: 1999-09-03
| PRIOR FLING DATE: 1999-09-03
| PRIOR FLING DATE: 1999-11-12
| PRIOR FLING DATE: 1997-11-27
| WHORE OF SEQ ID NOS: 4
| SEQ ID NO 3
| LENGTH: 10
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US-10-033-145-1924

US-10-033-145-1924

Sequence 1924, Application US/10033145

Publication No. US20020151515A1

Publication No. US20020151515A1

APPLICANT: GENERATION:

APPLICANT: GENERAR, BRINCE

APPLICANT: SHANKARA, BRINCE

APPLICANT: SHANKARA, BRINCAS

TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES

FILE REFERENCE: GAO201C

CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT PILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: PCT/US99/13800

PRIOR FILING DATE: 2001-11-05

SOFTWARE: PatentIn version 3.0

SOFTWARE: PatentIn version 3.0

LENGTH: 10
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches
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Pred. No. 45;
0; Mismatches
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Publication No. US20030078406A1
GENERAL INFORMATION:
APPLICANT: BLAIR, DONALD
APPLICANT: TOPOL, LILLA
APPLICANT: TOPOL, LILLA
APPLICANT: MARX, MARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
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US-10-033-145-1924
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CRGANISM: Homo sapiens
US-10-079-954-3
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TELEFAX: 650-903-3501
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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; ORGANISM: Mus musculus
US-10-314-322-312
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Description of Artificial Sequence:/No. US20030078406Ale = , OTHER INFORMATION: synthetic construct US-10-033-717-22
APPLICANT: CALOTHY, GEORGES
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DRM, A SECRETED PROTEIN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DRM, A SECRETED PROTEIN
FILE REFERENCE: 14014.0358
CURRENT APPLICATION NUMBER: US/10/033,717
CURRENT PILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-11-19
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-19
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: BARLIER FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: BARLIER FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: EASTER FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 38
LENGTH: 10
SEQ ID NO 22
LENGTH: 10
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Sequence 39, Application US/09796071

Patent No. US20020012925A1

GENERAL INFORMATION:

APPLICANT: Chee, Mark S.

IITLE OF INVENTION: Computer-Aided Visualization and Malysis System for Sequence Evaluation NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 83, Application US/10330627
Publication No. US2003017571A1
GENERAL INFORMATION:
APPLICANT: Volculescu, Victor E.
APPLICANT: Kinzler, Kenneth W
APPLICANT: Vogelstein, Bert
FILE REFERENCE: 001107.00319
CURRENT APPLICATION: HUMAN Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1564
SOPTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 83
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-330-627-83
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US-09-796-071-39
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US-10-330-627-83
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MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

CURRENT APPLICATION NATH:

APPLICATION NATHER: US/09/796,071

FILING DATE: 27-Feb-2001

CLASSIFICATION: UNKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: RELEEF NATHON:

REGISTRATION NUMBER: 36,653

REGISTRATION NUMBER: 36,653

REGISTRATION NUMBER: 36,653

TELEPHONE: 65-903-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 312, Application US/10314322
Publication No. US20030229911A1
GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILE REFERENCE: 000486.0016
CURRENT FILING DATE: 2002-12-09
FRICH APPLICATION NUMBER: US/0/074,737
PRIOR PRILING DATE: 1998-02-13
PRIOR PLING DATE: 1998-02-13
PRIOR PLING DATE: 1998-08-26
PRIOR FILING DATE: 1998-08-26
PRIOR FILING DATE: 1998-09-28
PRIOR FILING DATE: 1998-09-28
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-03-18
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ADDRESSEE: Ritter, Van Pelt & Yi LLP
STREET: 4906 BL Camino Real, Suite 205
CITY: Los Altos
STATE: California
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100.0%; Pred. No. 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
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Gaps
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Publication No. US20010034045A1
GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Ward, Michael
APPLICANT: Ward, Huaming
APPLICANT: Ward, Huaming
APPLICANT: Walkonen, Marid
TITLE OF INVENTION: Increased Production of Secreted
TITLE OF INVENTION: Proteins by Recombinant Eukaryotic Cells
TILE REFERENCE: GC590-2
CURRENT APPLICATION NUMBER: US/09/816,277
CURRENT FILING DATE: 2001-03-23
FRIOR APPLICATION NUMBER: US 09/534,692
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
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            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGIGTRATION NUMBER: 33,963
REGISTRATION NUMBER: 920010.426C2
TELEPHONE: (206) 682-6930
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 955:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7.8; DB
Pred. No. 53;
0; Mismatches
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; Sequence 4, Application US/10053526A
; Publication No. US20030003547A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Trichoderma reesei
US-09-816-277-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 GCTGGCACGCA 19
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US-09-816-277-62/c
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US-09-263-959-955
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                                                                                                                                                                                    Sequence 809, Application US/09263959
; Sequence 809, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Seatch
STREET: Sed and Berry LLP
STREET: Seat and Berry LLP
STREET: Good Columbia Center, 701 Fifth Avenue
COUNTRY: US
STREET: Washington
COUNTRY: US
STREET: RADABLE FORM:
MEDIUM TYPE: PLOPSY disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: OS-MAR-1999
FILING DATE: OS-MAR-1999
APPLICATION NUMBER: US/09/263,959
FILING DATE: OS-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 955, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
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  Gaps
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Pred. No. 53;
0; Mismatches ? " " " "
  Indels
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAXION FOR SEQ ID NO: 809:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
0; Mismatches
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
8; Conservative
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STRANDEDNESS: single
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                                           12 GGCACGCA 19
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Matches
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APPLICANT: Lyamichev.
APPLICANT: Lyamichev, Victor
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Alawi, Hatim T.
APPLICANT: Alawi, Hatim T.
APPLICANT: Takova, Tsetska
APPLICANT: Takova, Tsetska
APPLICANT: Neir, Bruce P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REPRESENT APPLICATION NUMBER: US/09/777,430A
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
SEQ ID NO 57
LENGTH: 12
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Sequence 78, Application US/10001670

Sequence 78, DS20030119002A1

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Rothberg, Jonathan

TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN

TITLE OF INVENTION: IDENTIFICATIONS THAT OCCUR IN POPULATIONS AND

TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

FILE REFERENCE: 7934-087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: Manoharan, Muthiah
APPLICANT: Bennett, Frank C.
TITLE OF INVENTION: Oligomuclectide Conjugates For Hepatic Delivery
FILE REFERENCE: Isis-5028
CURRENT APPLICATION NUMBER: US/10/080,979
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 11
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39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                          TYPE: DNA

) ORGANISM: Artificial Sequence

FATURE:

OTHER INFORMATION: Oligonucleotide

) NAME/KEY: misc_feature

; LOCATION: (6)..(6)

; COCATION: (6)..(6)

; UCCATION: (6)..(6)

; UCCATION: (6)..(10)
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Pred. No. 55;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Synthetic US-09-777-430A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 CGCTGGCACGC 18
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US-09-777-430A-57
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  INSTITUT CURIE; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (C.N.R.S.);
MUSEUM NATIONAL D'HISTOIRE NATURELLE; INSTITUT NATIONAL DE LA SANTE ET DE
RECHERCHE MEDICALE (INSERM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 106, Application US/10224836
Sequence 106, Application US/10224836
Sequence 106, Application US/2030862598A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
ATTILE OF INVENTION:
Modulating The Same
TILE OF INVENTION WORBER: US/10/224,836
CURRENT APPLICATION WUMBER: US/10/224,836
CURRENT FILING DATE: 2002-08-20
CURRENT FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 327
SOFTWARE: Pacentin version 3.1
SEQ ID NO 196
LIENGTH: 11
                                                                        APPLICANT: Durielx, Name
APPLICANT: But elsx, Name
APPLICANT: But of an elso applicant: Block Eloque
APPLICANT: But, Jian-Sheng
APPLICANT: Bier, Elodie
APPLICANT: Bergeas, Rosalie
APPLICANT: Feugeas, Jean-Paul
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EFFECTING HOMOLOGOUS RECOMBINATION
FILE REFERENCE: 3754/0x213
CURRENT APPLICATION NUMBER: D02-04-18
PRIOR PLING DATE: 2001-65-03
PRIOR PLING DATE: 2001-65-03
PRIOR FLING DATE: 2000-05-03
PRIOR FLING DATE: 2000-05-03
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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Pred. No. 53;
0; Mismatches 2; Indels
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Pred. No. 53;
2; Mismatches
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US-10-080-979-14/c
; Sequence 14, Application US/10080979
; Publication No. US20030191075A1
; PUBLICATION:
; APPLICANT: Cook, Philip Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-053-526A-4
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Best Local Similarity 63.6%;
Matches 7; Conservative
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 81.8%;
Matches 9; Conservative
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11 CGCTGGCCAGC 1
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US-10-001-670-79

US-10-001-670-79

Sequence 79, Application US/10001670

Publication No. US20030119002A1

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Nandabalan, Krishnan

TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND

TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND

TITLE OF INVENTION: US/10/01,670

CURRENT APPLICATION NUMBER: 09/231,303

PRIOR APPLICATION NUMBER: 09/231,303

PRIOR APPLICATION NUMBER: 08/663,824

PRIOR FILING DATE: 1996-06-14

NUMBER: PRIOR FILING USE: 1996-06-14

SOFTWARE: PRICE IN VET: 2.0

SEQ ID NO 79

LENTH: 1.2
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0
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; OTHER INFORMATION: Description of Artificial Sequence: linker
US-10-001-670-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: linker US-10-001-670-79
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Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 2; Indels
CURRENT APPLICATION NUMBER: US/10/001,670
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US-10-084-839-3010
; Sequence 3010, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chebak, LuAnne
; APPLICANT: Chebak, Michelle L.
; APPLICANT: Eis, Peggy S.
                     CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/231,303
PRIOR PILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 08/663,824
PRIOR PILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE PATENTIN Ver. 2.0
SEQ ID NO 78
LENGTH: 12
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A APPLICANT: Hall Jeff G.
A APPLICANT: Tp. 100.5.
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A APPLICANT: Tp. 100.5.
A APPLICANT: Tp. 100.5.
A APPLICANT: A Latent M. B. APPLICANT: A LATENT M. APPLICANT M. WARREN: O10410.2

A CHARLES A LATENT M. APPLICANT M. WARREN: O10410.2

A PRIOR A PLINCANT M. WARREN: O10410.2

B PRIOR A PLINCANT M. APPLICANT M. WARREN: O10410.2

B PRIOR
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| Sequence 2287, Application US/09989789 | Patent No. US20020063379A1 | Sequence 2287, Application US/09989789 | Patent No. US20020063379A1 | GENERAL INFORMATION: | APPLICANT LIV, Oiang | TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE | TITLE OF INVENTION: PINIBLES BY ZINC FINGERS | FILE REPERSENCE: 8125-0011.20 / 811-US2 | CURRENT PAPLICATION NUMBER: US/09/989, 789 | CURRENT FILING DATE: 2002-03-25 | NUMBER OF SEQ ID NOS: 4085 | SEQ ID NO 2287 | LENGTH: 10 | SEQ ID NO 2287 | LENGTH: 10 | SEQ ID NO 2287 | LENGTH: 10 | LENGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-789-2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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US-09-990-186-2286
                                                          US-09-989-789-2287
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                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT LIU, Q1300
APPLICANT: LIU, Q1300
APPLICANTON: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / $11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT PILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2216
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| Sequence 2286, Application US/09989789
| Patent No. US20020063379A1
| GENERAL INFORMATION:
| APPLICANT: LIU, Qiang
| TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
| TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
| FILE REPERENCE: 8325-0011.20 / S11-US2
| CURRENT APPLICATION NUMBER: US/09/989, 789
| CURRENT FILING DATE: 2002-03-25
| NUMBER OF SEQ ID NOS: 4085
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 2286
| LENGTH: 9
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Pred. No. 3.3e+02;
0; Mismatches 1; Indels
                                                                                                     DB 1; Length 12;
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Pred. No. 3.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                   2; Indels
                                                                                                 Score 7.8; DB
Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2216, Application US/09989789 Patent No. US20020063379A1
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88.9%;
; OTHER INFORMATION: Primer tail US-10-312-273-663
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88.9%;
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ORGANISM: Artificial Sequence
PEATURE:
                                                                                                 Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.>
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US-09-989-789-2286
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Gaps

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Score 7.4; DB 1; Length 9; Pred. No. 3.3e+02; 0; Mismatches 1; Indels

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                                                                   RESULT 87
US-09-196-116.
US-09-196-116.

US-09-99-1186-2216

Sequence 2216, Application US/09990186

Publication No. U520030068675A1

GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

TITLE OF INVENTION: US/09/990.186

CURRENT FILING DATE: 2001-11-20

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2216

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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| Publication No. US20030068675A1
| CENERAL INFORMATION:
| APPLICAT: LIU, Olang
| TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
| TITLE FERENCE: 8325-0011.21 / 811-US3
| CURRENT APPLICATION NUMBER: US/09/990,186
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Pred. No. 3.3e+02;
0; Mismatches 1; Indels
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88.9%;
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37.0
Best Local Similarity 88.5
Matches 8; Conservative
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1 ATGGACTTG 9
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1 Arggacrig 9

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RESULT 93 ઠ ö ö RESULT 90
US-09-989-994-2216

Sequence 2216, Application US/09989994

Publication No. US2030104526A1

GENERAL INFORMATION:

APPLICANT: LIU, Qiang

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / 811-US2

CURRENT APPLICATION NUMBER: US/09/989,994

CURRENT FILING DATE: 2001.11-20

NUMBER OF SEQ ID NOS: 4085

SOFTWARE PATENT NOS: 4085

SOFTWARE PATENT NOS: 2.06

BENGTH: 9 Sequence 2287, Application US/0990186
FUDIcation No. US2030068675A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSTITON DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8328-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT APPLICATION NUMBER: US/09/990,186
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2287
LENGTH: 9
TYPE: DNA OTHER INFORMATION: DEscription of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-994-2216) OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-990-186-2286 OCGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: example target OTHER INFORMATION: DNA US-09-990-186-2287 0; Gabs Gabs ; 0 Length 9; Length 9; 1; Indels 1; Indels Score 7.4; DB 1; Pred. No. 3.3e+02; 0; Mismatches 1. Score 7.4; DB 1; Pred. No. 3.3e+02; 0; Mismatches 1 CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2286
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence 37.0%; 88.9%; TYPE: DNA ORGANISM: Artificial Sequence FEATURE: Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative Query Match
Best Local Similarity 88.9
Matches 8; Conservative 1 ATGGACTCG 9 1 ATGGACTCG 9 1 ATGGACTTG 9 RESULT 89 US-09-990-186-2287 셤

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RESULT 91
US-09-998-994-2286

Sequence 2286, Application US/09989994

Publication No. US20030104526A1

GENERAL INFORMATION:

APPLICANTY: LIU, Giang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REPERRNCE 8325-0011.20 / S11-US2

CURRENT AFPLICATION NUMBER: US/09/989, 994

CURRENT FILING DATE: 2001-11-20

NUMBER OF SEQ ID NOS: 4085

SOFTWARE PACENTIN Ver. 2.0

SEQ ID NO 2286

LENGTH: 9
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OTHER INFORMATION: Description of Artificial Sequence: example target
OTHER INFORMATION: DNA
US-09-994-2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2287, Application US/0998994
Publication No. US20030104526A1
GENERAL INFORMATION:
APPLICAMY: LIU, Qiang
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
CURRENT APPLICATION UNMER: US/09/989,994
CURRENT APPLICATION UNMER: US/09/989,994
CURRENT APPLICATION UNMER: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2287
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Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.0%; Score 7.4; DB 1; Length 9; Best Local Similarity 88.9%; Pred. No. 3.3e+02; Matches 8; Conservative 0; Mismatches 1; Indels
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US-09-989-994-2287
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Length 9; Indels

Score 7.4; DB 1; Pred. No. 3.3e+02; 0; Mismatches 1.

Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative

PU02 54:25:21 0

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APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri TITLE OF INVENTION: Proteins, Genes and Their Use for TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer FILE NEFERBNCE: 2543-1026
CURRENT FILING DATE: 2002-02-13
CURRENT FILING DATE: 1099-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 2000-03-30
SPIOR APPLICATION NUMBER: PCT/GB00/03143
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 351
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20010029015A1

JEGENERAL INFORMATION:

APPLICANT: Ozcilus, Laurie J.

APPLICANT: Ozcilus, Laurie J.

APPLICANT: Ozcilus, Laurie J.

TITLE OF INVENTION: TORSIN, TORSIN, ELATED GENES, AND TITLE OF INVENTION: TORSIN, TORSIN, DISEASES FILE REFERENCE: 0838.1001009

TITLE OF INVENTION: WHERER: US/09/772,105

CURRENT APPLICATION NUMBER: US 09/218,363

PRIOR PLING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

NUMBER OF SEQ ID NOS: 90

SOFTWARE FREEDOM NUMBER: US 08/050,244

PRIOR FILING DATE: 1997-06-19

NUMBER OF SEQ ID NOS: 90

LENGTH: 10

LENGTH: 10
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Best Local Similarity 88.9%; Pred. No. 59;

Matches 8; Conservative 0; Mismatches 1; Indels
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37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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COTHER INFORMATION: Exon/intron of TORB US-09-772-105-80
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Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-10-076-047A-67
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ORGANISM: Unknown
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US-10-096-596-15/c

Sequence 15, Application US/10096596

Publication No. US20030049653A1

GENERAL INFORMATION:
APPLICANT: Kinzler, Kenneth W
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Witcor
APPLICANT: APPLICANT: Volculescu, Victor
APPLICANT: APPLICANT: Volculescu, Victor
APPLICANT: APPLICATION NUMBER: US/10/096,596
CURRENT APPLICATION NUMBER: US/00/096,596
CURRENT APPLICATION NUMBER: US 08/544,861

PRIOR PILING DATE: 1995-09-12

PRIOR FILING DATE: 1995-09-12

PRIOR FILING DATE: 1995-00-18

PRIOR FILING DATE: 1995-10-18

PRIOR FILING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR PRILING DATE: 1995-10-18

PRIOR PRILING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR PRILING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR PRILING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR APPLICATION NUMBER: US 09/107,228

PRIOR APPLICATION NUMBER: US 09/107,228

PRIOR PRILING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR PRILING DATE: 1995-10-18

PRIOR PLING DATE: 1995-10-18

PRIOR PRILING DATE: 1995-10-18
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US-10-076-047A-65/C

Sequence 65, Application US/10076047A

Sequence 65, Application US/10076047A

Sequence 67, Application US/10076047A

Sequence 67, Application No. US20010152935A1

GENERAL INFORMATION:
TITLE OF INVENTION: Proteins, Genes and Their Use for TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer; TITLE OF INVENTION WUMBER: GB 9919258.5

PRIOR PILING DATE: 1999-08-13

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-30

PRIOR PILING DATE: 2000-08-14

NUMBER OF SEQ ID NOS: 351

SEQ ID NOS: 351

SEQ ID NOS: 
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US-10-076-047A-67/c
Sequence 67, Application US/10076047A
; Publication No. US20030152935A1
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Best Local Similarity 88.5
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-10-096-596-15
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ORGANISM: Homo sapiens
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READABLE FORM:
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US-09-989-789-568/C
Sequence 568, Application US/09989789
Fatent No. US20020063379A1
GENERAL INFORMATION:
FAPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPREBENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT PILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SSOFTWARE: Patentin Ver. 2.0
SEQ ID NO 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: example target
OTHER INFORMATION: DNA
OTHER INFORMATION: DNA
US-09-989-789-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-567
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE TITLE OF INVENTION: TAIPLETS BY ZINC FINGERS FILE REPERENCE: 8125-0011.20 / S11-US2 CURRENT APPLICATION NUMBER: US/09/989,789 CURRENT PILING DATE: 2002-03-25 NUMBER OF SEQ ID NOS: 4085 SSCTWARE: Patentin Ver. 2.0 LENGTH: 10
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Pred. No. 59;
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Pred. No. 59;
0; Mismatches 1; Indel8
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Fatent No. US20020137910A1
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pline Street
CITY: San Francisco
STREET: California
COUNTRY: USA
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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88.9%;
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                           37.0%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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US-09-772-719-21/c
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; Sequence 567, Application US/09990186
; Sequence 567, Application US/09990186
; Publication No. US200300686/5A1
; Publication No. US200300686/5A1
; Publication No. US200300686/5A1
; PITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: PRIPLETS BY ZINC FINGERS
; TITLE OF INVENTION: UNMERS: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PATENTING DATE: 2001-11-20
; SEQ ID NO 567
; LENGTH: 10
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COMPUTER READABLE FORM:

MEDIUTER TEBLES FORM:

MEDIUTER: IBM FC compatible

COMPUTER: IBM FC compatible

COMPUTER: IBM FC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/772,719

FILING DATE: 30-JAN-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,049

FILING DATE: 07-UN-1995

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-UN-1994

ATTORNAYAGENT INFORMATION:

NAME: Lauder, Leona L.

REJERRATION NUMBER: D-0021.3E

TELEFORM INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFORM: 415-981-2034

TELEFORM GHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels
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DESCRIPTION: p53 binding site
PUBLICATION INFORMATION:
AUTHORS: B1 Deiry et al.
TITLE: "Human genomic DNA sequences define a
TITLE: consensus binding site for p53"
VOLUME: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7.4; DB
Pred. No. 59;
0; Mismatches
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
OTHER INFORMATION: DNA
US-09-989-994-567
          Sequence 567, Application US/0998994
Publication No. US20030104526A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / 811-US2
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085.
SOFTWARE: Patentin Ver. 2.0
   JS-09-989-994-567/C
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CHER INFORMATION: Description of Artificial Sequence: example target
CHER INFORMATION: DNA
US-09-990-186-568
                                                                                                                                        Sequence 568, Application US/09990186
Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICAMT: LIU, Qiano
TITLE OF INVENTION:
FILE REPRENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 568
LENGTH: 10
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Pred. No. 59;
0; Mismatches 1; Indels
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels
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PUBLICATION NO. US20030099945A1
GENERAL INFORMATION:
APPLICANT: Eaton, Bruce
APPLICANT: Tarasow, Theodore
ITITLE OF INVENTION: Parallel Selex
FILE REFERENCE: 2636-108-C.II
CURRENT APPLICATION NUMBER: US/09/916,443A
FILER REPERENCE: 2636-108-C.II
CURRENT APPLICATION NUMBER: US 09/546,657
PRIOR APPLICATION NUMBER: US 09/546,657
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1996-03-20
PRIOR APPLICATION NUMBER: US 08/618,700
PRIOR FILING DATE: 1996-03-20
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88.9%;
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Best Local Similarity 88.5
Matches 8; Conservative
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CGCTGCCAC 1
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US-09-916-443A-1
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37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 59; tive 0; Mismatches 1; Indels

Best Local Similarity 88.5 Matches 8, Conservative

Query Match

SEQ ID NO 567

8 CGCTGGCAC 16

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                                                                                   US-09-99-994-568/c

| Sequence 568, Application US/0998994
| Sequence 568, Application US/0998994
| Publication No. US20030104526A1
| GENERAL INFORMATION:
| APPLICANT: LIU, Qiang
| TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
| TITLE OF INVENTION: PRIPLETS BY ZINC FINGERS
| TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
| TITLE OF INVENTION: 2011.20 / $11.052
| CURRENT FILING DATE: 2001.11-20
| NUMBER OF SEQ ID NOS: 4085
| SOFTWARER PATENTION VET. 2.0
| SEQ ID NO 568
| LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: example target COTHER INFORMATION: DNA US-09-989-994-568
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 9; Conservative 0; Mismatches 1; Indels
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US-10-257-021-109/C
is Sequence 109, Application US/10257021
is Publication No. US20030211498A1
is GENERAL INFORMATION:
is APPLICANT: Morin, Parrice J.
is APPLICANT: Sherman-Baust, Cheryl A.
is APPLICANT: Pizer, Ellen S.
is APPLICANT: Hough, Colleen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Gaps

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37.0%;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-10-033-145-546
    ; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-475
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; ORGANISM: Homo sapiens
US-10-033-145-479
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US-10-033-145-479
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LENGTH: 10
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Sequence 475, Application US/10033145

Publication No. US20020151531

GENERAL INFORMATION:
APPLICANT: GENERALS CREPARATION
APPLICANT: GENERALS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GAO201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT APPLICATION NUMBER: DS/00-11-05
PRIOR FILING DATE: 1999-66-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: PATECHIL VEFSION 3.0
SEQ ID NO 475
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) Publication No. US200201515541
) FURBEAL INFORMATION:
APPLICANT: GENERAL SERVICE
APPLICANT: STANKARA, SILNIVAS
ITILE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GAZOLC
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin version 3.0
LENGTH: 10
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Pred. No. 59;
0; Mismatches 1; Indels
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TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER CURERT APPLICATION NUMBER: US/10/257,021
CURRENT APPLICATION NUMBER: US/10/257,021
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10947
PRIOR RILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2000-04-03
SPIOR APPLICATION NUMBER: 60/194,336
PRIOR PILING DATE: 2000-04-03
SOFTWARE: PRESEQ for Windows Version 4.0
SOFTWARE: PRESEQ for Windows Version 4.0
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Pred. No. 59;
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88.9%;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.5
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-10-033-145-133
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                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-10-257-021-109
                                                                                                                                                                                                                                                                                                                                                                                               11 TGGCACGCA 19
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US-10-033-145-475/c
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US-10-033-145-133
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Sequence 546, Application US/10033145

Publication No. US200201515151

GENERAL INFORMATION:
APPLICANT: GENERIS, ERUCE
APPLICANT: GENERIS, ERUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GAOJOLC
CURRENT APPLICATION NUMBER: US/10/033,145

CURRENT PILING DATE: 2001-11-05
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137

SOFTWARE: Patentin version 3.0

LENGTH: 10

LENGTH: 10
                                                                                                                                                                                                                                                                 Sequence 479, Application US/10033145
Publication No. US20020151515A1
GENERAL INFORMATION:
APPLICANT: GENERAL:
APPLICANT: GENERES, BRUGE
APPLICANT: SCHAWARA, SRINUVAS
TITLE OF INVENTION: PERPERATION AND USE OF SUBERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR APPLICATION NUMBER: PCT/US99/13800
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin version 3.0
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DB 1; Length 10,
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                                                 1; Indels
Score 7.4; DB
Pred. No. 59;
0; Mismatches
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Pred. No. 59;
0; Mismatches
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Tue Jun 8 12:32:43 2004
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RESULT 113
US-10-330-627-656
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; Publication No. US202015151511
; Publication No. US20201515151
; GENERAL INFORMATION:
    APPLICANT: GENZYME CORPORATION
; APPLICANT: GENZYME CORPORATION
; APPLICANT: SHAWKARA, SRINIVAS
; TILLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; TILLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; TILLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; CURRENT FILING DATE: 2001-11-05
; PRIOR PAPLICATION NUMBER: US/10/033,145
; PRIOR PELLING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1224
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Sequence 567, Application US/10033145
Publication No. US/2020151515A1
GENERAL INFORMATION:
APPLICANT: GENERYE CORPORATION
APPLICANT: SHANGARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REPRENCE: A20201
CURRENT FILING DATE: 2001-11-05
PRIOR PELING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE PARENTE PREPARE: POTYUS99/13800
SPINGRE PARENTE PARENTE 1299-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE PARENTE PARENTE 130-06
SOFTWARE PARENTE PARENTE 130-06-18
NUMBER OF SEQ ID NOS: 2137
SEQ ID NO 567
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Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels
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Pred. No. 59;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative C
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CORGANISM: Homo sapiens
US-10-033-145-1224
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US-10-033-145-567
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2 TGGCAGGCA 10
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US-10-330-627-693

Sequence 693, Application US/10330627

Publication No. US20030175771A1

GENERAL INFORMATION:

APPLICANT: Velculescu, Victor E.

APPLICANT: Velculescu, Victor E.

APPLICANT: Vogelstein, Bert

TITLE OF INVENTION: Human Transcriptomes

FILE REFERENCE: 001107.00319

CURRENT APPLICATION NUMBER: US/10/330,627

CURRENT PPLICATION NUMBER: US 09/448,480

PRIOR FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 1564

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 693

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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PUDLication No. US200330175771A1
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT RILING DATE: 2002-12-30
FRICK PILICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 656
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TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT PELLOR INVENER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR PILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 357
LENGTH: 10
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Best Local Similarity 88.9
Matches 8; Conservative
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; ORGANISM: Homo sapiens
US-10-330-627-656
                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-330-627-357
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Best Local Similarity
Matches 8; Conserv
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Query Match
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels
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US-10-330-627-1368
Sequence 1368, Application US/10330627
Publication No. US2003017571A1
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor E.
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Vogelstein, Bert
ITILE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 1368
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US-J0-330-627-1227

VS-Quence 1227. Application US/10330627

Sequence 1227. Application US/10330627

PUBLICATION: OS US2030175771A1

APPLICANT: Velculescu, Victor E. APPLICANT: Vogelstein, Bert

TITLE OF INVENTION: Human Transcriptomes

FILE REPERENCE: 001107.00318

CURRENT APPLICATION NUMBER: US/10/330,627

CURRENT FILING DATE: 2002-12-30

PRIOR PILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 1564

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1227
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Sequence 97, Application US/10197019
Fublication No. US20030207284A1
GENERAL INFORMATION:
APPLICANT: Chew, Anne
APPLICANT: Denton, R. Rex
APPLICANT: Gilson, Christopher Raleigh
APPLICANT: Nandabalan, Krishnan
APPLICANT: Parks, Katie E.
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-10-330-627-1227
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CORGANISM: Homo sapiens
US-10-330-627-1368
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88.9%; Pred. No. 59;
tive 0; Mismatches 1; Indels
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                               37.0%; Score 7.4; DB 1; Length 10;
88.9%; Pred. No. 59;
tive 0; Mismatches 1; Indels
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Sequence 1226, Application US/10330627
Sequence 1226, Application US/10330627
SENERAL INFORMATION:
APPLICANT: Volculescu, Victor E.
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Human Transcriptomes
TITLE REPERBNG: 001107, 00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT PILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTHARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 1226
LENGTH: 10
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION

PUBLICATION NO. US20030175771A1

GENERAL INFORMATION

APPLICANT: Velculescu, Victor E.

APPLICANT: Kinzler, Kenneth W

APPLICANT: Wogelstein, Bert

TITLE OF INVENTION: Human Transcriptomes

FIER REFERENCE: 001107. 00319

CURRENT APPLICATION NUMBER: US/10/330,627

CURRENT FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 1564

NUMBER OF SEQ ID NOS: 1564

SEQ ID NO 1122

LENGTH: 10
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                    Best Local Similarity 88.9
Matches 8; Conservative
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, ORGANISM: Homo sapiens
US-10-330-627-1122
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CRGANISM: Homo sapiens
US-10-330-627-1226
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; ORGANISM: Homo sapiens
US-10-330-627-693
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US-10-330-627-1226
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US-10-330-627-1122
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US-10-197-019-98

US-10-197-019-98

Sequence 98, Application US/10197019

Publication No. US20030207284A1

GENERAL INFORMATION:
APPLICANT: Chew, Anne
APPLICANT: Gilson, Christopher Raleigh
APPLICANT: Gilson, Christopher Raleigh
APPLICANT: Parks, Kathe E.
ITLE OF INVENTION: HAPLOTYPES OF THE UCP2
CURRENT FILE OF INVENTION: HAPLOTYPES OF THE UCP2
CURRENT FILING DATE: 2002-07-16
PRIOR PILLING DATE: 2002-07-16
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEC ID NOS: 116
SEC ID NO 98
LENGTH: 10

LENGTH: 10

LENGTH: 10
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US-10-193-507-83/c
; Sequence 83, Application US/10193507
; Publication No. US20040018493A1
; GENERAL INFORMATION:
; APPLICANT: Ansatasio, Alison E.; APPLICANT: Kazemi, Amir
; APPLICANT: Palon, Vicente
; APPLICANT: Banh, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE
; FILE REFRENCE: WHAPLOTYPES OF THE CD3E GENE
; CURRENT APPLICATION NUMBER: US/10/193,507
; CURRENT PILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/304,573
; NUMBER OF SEQ ID NOS: 86
TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
FILE REPERENCE: WFH-0042US
CURRENT APPLICATION NUMBER: US/10/197,019
CURRENT FILING DATE: 2002-07-16
FRIOR APPLICATION NUMBER: PCT/US01/02485
FRIOR PILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin version 3.1
LENGTH: 10
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Pred. No. 59;
0; Mismatches
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37.0%; Score 7.4; DB
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-97
                                                                                                                                                                                                                                                                                                                                                                            6 CTCGCTGGC 14
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; ORGANISM: Homo sapiens
US-10-197-019-98
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RESULT 122
US-10-642-322-20/c

Sequence 20, Application US/10642322

Publication No. US20040077080A1

GENERAL INFORMATION:

APPLICANT RAUCY, JUdy

TITLE OF INVENTION: Composition and Methods for Induction of Proteins Involved in TITLE OF INVENTION: Achobictic Metabolism

TITLE OF INVENTION: Achobictic Metabolism

FILE REPREBACE: UN-00114-P.1.1.1.1

CURRENT APPLICATION NUMBER: US/10/642,322

CURRENT FILING DATE: 2002-08-15

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-10-11

PRIOR FILING DATE: 2000-10-17

NUMBER OF SEQ ID NOS: 37

SEQ ID NO 20

LENGTHARE PARENTIN VERSION 3.2
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Sequence 22, Application US/10642322

JUBILATION NO. US20040077080A1

GENERAL INFORMATION:
JAPPLICANT: Raucy, Judg,
TITLE OF INVENTION: Composition and Methods for Induction of Proteins Involved in
TITLE OF INVENTION: Xenobiotic Metabolism

FILE REPRENCE: PUR-00114-P.1.1.1.1.

CURRENT PILING DATE: 2003-08-16

PRIOR APPLICATION NUMBER: US 09/832,621

PRIOR APPLICATION NUMBER: US 60/196,681

PRIOR APPLICATION NUMBER: US 60/196,681

PRIOR PELING DATE: 2000-04-12

PRIOR PELING DATE: 2000-04-12

PRIOR FILING DATE: 2000-10-17
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Pred. No. 59;
0; Mismatches 1; Indels
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Pred. No. 59;
0; Mismatches 1; Indels
; SOFTWARE: PatentIn version 3.1; SEQ ID NO 83
; LENGTH: 10
; TYPE: DNA
; ORGANIEM: Homo sapiens
US-10-193-507-83
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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CORGANISM: Homo sapiens
US-10-642-322-20
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Sequence 89, Application US/09249155

Publication No. US2030037345A1

GENERAL INFORMATION:

APPLICANT: Heber-Katz, Ellen

TITLE OF INVENTION: Compositions and Methods for Mound

TITLE OF INVENTION: Compositions and Methods for Mound

TITLE OF INVENTION: Healing

FILE REPERENCE: 00486.78503

CURRENT APPLICATION NUMBER: 06/074,737

EARLIER APPLICATION NUMBER: 60/074,737

EARLIER APPLICATION NUMBER: 60/097,937

EARLIER FILING DATE: 1998-08-26

EARLIER FILING DATE: 1998-09-26

EARLIER FILING DATE: 1998-09-26

EARLIER FILING DATE: 1998-09-28

NUMBER: OF SEO ID NOS: 254
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TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
FILE REPEABLE: 00486.78503
CURRENT PELLING DATE: 1999-02-12
EARLIER APPLICATION NUMBER: 60/074,737
EARLIER APPLICATION NUMBER: 60/074,737
EARLIER APPLICATION NUMBER: 60/097,937
EARLIER PILING DATE: 1998-08-26
EARLIER FILING DATE: 1998-08-26
EARLIER FILING DATE: 1998-08-26
EARLIER FILING DATE: 1998-08-26
EARLIER FILING DATE: 1998-08-26
SOFTWARE OF SEQ ID NOS: 254
SOFTWARE FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 254
SOFTWARE FELLING DATE: 1998-09-18
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Pred. No. 63;
0; Mismatches
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Publication No. US20030037345A1
GENERAL INFORMATION:
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Best Local Similarity 88.9%;
Matches 8; Conservative (
                                                                                                                                                 Query Match 37.0
Best Local Similarity 88.9
Matches 8; Conservative
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo Bapiens
US-10-642-322-22
                                                                                                                                                                                                                                                 11 TGGCACGCA 19
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CORGANISM: Mus musculus
US-09-249-155-89
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Sequence 175703, Application US/10027632

Publication No. US2020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nuclectide

FILE REPERENCE: 108627.129

CURRENT PILING DATE: 2002-04-30

FRIOR PILING DATE: 2002-04-30

FRIOR PILING DATE: 2000-07-12

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-02-34

FRIOR FILING DATE: 2000-02-34

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-08-09

FRIOR FILING DATE: 1999-08-09
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Query Match 37.0%; Score 7.4; DB 1; Length 11; Best Local Similarity 89.9%; Pred. No. 63; Matches 8; Conservative 0; Mismatches 1; Indels
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APPLICANT: Bard CO. COLL
APPLICANT: Bard CO. COLL
APPLICANT: Renneth Rinzler
TITLE OF INTENTION: BUDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT PILING DATE: 2001-08-01
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-11
SEQ ID NO 9: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LEAGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-9
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Query Match
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US-10-027-632-175703/C
Sequence 175703, Application US/10027632
Publication No. US20030204075A9
Sequence 175703, Application US/10027632
Publication No. US20030204075A9
Sequence 175703, US20030204075A9
SEQUENCAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US/10/027,632
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-04-20
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/198,78
FRIOR APPLICATION NUMBER: US 60/198,78
FRIOR APPLICATION NUMBER: US 60/198,78
FRIOR PILING DATE: 1999-11-28
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1
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; Sequence 17712, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
    APPLICANT WANG, David G.
    TITLE OF INVENTION: Polymorphisms in the Human Genome
    TITLE OF INVENTION: Polymorphisms in the Human Genome
    TITLE OF INVENTION: Polymorphisms in the Human Genome
    TITLE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
    PRIOR FILING DATE: 2000-04-20
    PRIOR FILING DATE: 2000-04-20
    PRIOR FILING DATE: 2000-04-20
    PRIOR FILING DATE: 2000-04-20
    PRIOR FILING DATE: 2000-03-29
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llarity 88.9%; Pred. No. 63;
Conservative 0; Mismatches
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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US-10-027-632-175712/c
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; ORGANISM: Human
US-10-027-632-175703
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175703
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WESULI 1312, Application US/10027632

Sequence 17512, Application US/10027632

SEQUENCE 17512, Application US/20030204075A9

SENDIAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Delymorphisms in the Human Genome
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/166,002

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FEASER FEASER FOR Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-02-28
PRIOR FILING DATE: 1999-00-28
PRIOR FILING DATE: 1999-00-3
PRIOR FILING DATE: 1999-08-09
SOFTWARE: PSECSIO NOS: 325720
SOFTWARE: PSECSIO FOR WINDOWS Version 4.0
SEQ ID NO 175712
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88.9%; Pred. No. 63;
Live 0; Mismatches
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88.9%; Pred. No. 63;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8, Conservative
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; ORGANISM: Human
US-10-027-632-175712
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ORGANISM: Human
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| DS-10-14-3-24-1//C
| Publication No. US20030229911A1
| GENERAL INFORMATION:
| APPLICANT: Heber-Katz, Ellen
| TITLE OF INVENTION: Compositions and Methods for Wound
| TITLE OF INVENTION: Healing
| FILE REFERENCE: 000486.0016
| CURRENT FILING DATE: 2002-12-09
| FRIOR APPLICATION NUMBER: US 60/074,737
| PRIOR FILING DATE: 1998-02-13
| PRIOR FILING DATE: 1998-02-13
| PRIOR FILING DATE: 1998-02-26
| PRIOR FILING DATE: 1998-02-12
| PRIOR FILING DATE: 1998-02-26
| PRIOR FILING DATE: 1998-02-12
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IIILE OF INVENTION: Compositions and Methods for Wound IIILE OF INVENTION: Healing
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37.0%; Score 7.4; DB:
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches
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                                                  FILE REFERENCE: 000486.00116
CURRENT APPLICATION NUMBER: US/10/314,322
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/074,737
PRIOR FILING DATE: 1988-02-13
PRIOR FILING DATE: 1988-02-65
PRIOR FILING DATE: 1998-09-26
PRIOR FILING DATE: 1998-09-28
PRIOR PILING DATE: 1998-09-28
PRIOR PILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: US 09/249,155
PRIOR PILING DATE: 1998-02-12
NUMBER OF SEQ ID NOS: 346
SOFTWARE: FESTERG for Windows Version 4.0
SEQ ID NO 89
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Job time : 0.001 secs
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Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
) ORGANISM: Mus musculus
US-10-314-322-89
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; ORGANISM: Mus musculus
US-10-314-322-177
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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8, 2004, 12:32:21 ; Search time 0.001 Seconds (without alignments) 2.160 Million cell updates/sec June Run on:

- nucleic search, using sw model

OM nucleic

US-10-003-919-21 20

Title: Perfect score:

1 ATGGACTCGCTGGCACGCAC 20 Scoring table: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 5 segs, 54 residues Searched:

10 Total number of hits satisfying chosen parameters:

length: 0 length: 200000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 5 summaries

rstdb:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	ACCESSION: AZ972315	ACCESSION: CF307276	ACCESSION: CF307431	ACCESSION: CF297970	ACCESSION: CF330558
		Ω	1 AZ972315	CF307276	CF307431	CF297970	CF330558
		8	н	н	Н	Н	Н
		Match Length DB ID	20	σ	σ	ω	80
ю	Query	Score Match	13.8 69.0	32.0	32.0	27.0	27.0
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	Result	No.		7	ო	4	ın
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ALIGNMENTS

Own musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmanila; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Lo 20)

B Dunn,D, Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.,

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

L Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah AZ972315 20 bp DNA linear GSS 27-APR-2001 2M0246E09F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0246E09 F, genomic survey sequence. AZ972315.1 GI:13843542 GSS. VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS JOURNAL COMMENT RESULT 1 AZ972315 LOCUS ACCESSION TITLE

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor or oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XL10-GG1d (Stratagene) cells
and selected for ampicillin resistance." Ë ö /sex="Female" /lab host="E. coli strain XLIO-Gold, Tl-resistant, F-" /lone lib="Mouse 10kb plasmid UUGC2M library" /noce="PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson SLC, Gaps Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., .. 0 Score 13.8; DB 1; Length 20; Pred. No. 0; Mismatches 2; Indels A112, USA
Tel: 801 585 5606
Fax: 801 585 717
Email: ddunndegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0246 row: E column: 09
Sq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers 1. .20 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0246E09" . 4 GACTCGCTGGCACGCAC 20 69.0%; Query Match
Best Local Similarity 88.2
Matches 15; Conservative source FEATURES

2 daarceceedcacecac 18 RESULT 2 CF307276 à

Dryza sativa

Oryza sativa

Oryza sativa

Dukaryota; Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

E (hasses 1 to 9)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

L Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193 CF307276 9 bp mRNA linear EST 15-AUG-2003 HDA1--06-D23.gl OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--06-D23, mRNA CF307276 CF307276.1 GI:33679037 sequence ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION JOURNAL COMMENT REFERENCE AUTHORS TITLE

OM nucleic - nucleic search, using sw model

June 8, 2004, 12:28:06; Search time 0.001 Seconds (without alignments) 77.840 Million cell updates/sec Run on:

US-10-003-919-21 20 1 ATGGACTCGCTGGCACGCAC 20

Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

178 segs, 1946 residues

Searched:

356

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 178 summaries

rnidb:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΩI	-09-798-	ņ	-08-845-021-31	-998-60-	-09-081-646-637	-09-371-772B-	-09-176-3	-09-474-432B-1	-09-476-387-14	-08-363-2	-08-363-240A-2	-08-872-417B	US-09-436-518-3	3-584-040-8	US-09-371-772B-4143	-647-344A-	-08-929-8	18-929-	-08-574-396-4	J8-544-381B	-09-156-828B-	-08-973-568-4	-08-778-794A-	-09-306-653-2	-09-306-653-3	-09-306-653-3	-09-306-653-3	-09-306-653-4	-09-306-653-4	-09-621-27	-09-621-275-4	JS-09-621-275-45
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US-09-621-275- US-09-621-275- US-08-547-214- US-08-547-214- US-08-663-8238 US-08-942-406- US-08-942-406- US-09-322-617- US-09-322-617- US-09-203-2318 US-09-203-2318 US-09-203-2318 US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561- US-09-751-561-	US-08-28-2 US-08-480-4738-2 US-08-915-217-2 US-08-915-217-2 US-08-859-954-1 US-08-859-954-1 US-08-430-536-1 US-08-430-536-1 US-08-430-536-1 US-08-68-280-1 US-08-68-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-280-1 US-08-98-1 US-08-381-471B-1 US-08-381-471B-1 US-08-381-471B-1 US-08-381-441B-1	1 US-09-308-984-3 1 US-09-313-221A-132 1 US-09-313-221A-132 1 US-08-327-525A-3 1 US-08-327-525A-39 1 US-08-531-1378-39 1 US-09-196-071-39 1 US-09-796-071-39 1 US-08-929-856-5 1 US-08-929-856-5 1 US-08-929-856-5 1 US-08-928-95-6 1 US-08-928-95-7 1 US-08-928-95-7 1 US-08-97-98-98-98-98-98-98-98-98-98-98-98-98-98-	US-08-170-290A-11 US-08-309-245-1 US-08-309-245-1 US-08-463-101-1 US-08-463-101-1 US-08-461-410B-4 US-08-461-410B-4 US-08-481-65BB-21 US-08-481-65BB-21 US-08-481-65BB-21 US-08-481-65BB-21 US-08-481-65BB-21 US-08-481-65BB-21 US-08-481-65BB-21 US-08-388-353-704 US-08-388-353-704 US-08-388-353-704 US-08-388-353-704
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RESULT 1
US-09-798-096-15/c

j Sequence 15, Application US/09798096

j Patent No. 6399378

j GENERAL INFORMATION:
    APPLICANT: Domna T. Wart
    TILE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
    TILE OF INVENTION: ANTISENSE: US/09/798,096
    CURRENT FILING DATE: 2001-03-01
    NUMBER OF SEQ ID NOS: 89
    LENGTH: 20
    LENGTH: 20
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US-09-143-212-59/c
US-09-143-212-59/c
Sequence 59, Application US/09143212B
Patent No. 6077672
GENERAL INFORMATION:
APPLICANT: Brett P. Monia and Lex M. Cowsert
ITILE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
FILE REPERBENCE: RTS-0005
CURRENT APPLICATION UNMBER: US/09/143,212B
CURRENT FILING DATE: 1998-08-28
NOWHER OF SEQ ID NOS: 87
SEQ ID NO 59
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%; Pred. No. 7;
Matches 15; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-08-849-021-31/C
; Sequence 31, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
APPLICANT: MORGANTE, MICHELE
APPLICANT: MORGANTE, JULIE M.
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-59
                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-798-096-15
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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18 TGGACTCGCTGGC 6
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CURRENT FILING DATE: US/09/866,108A

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PLILAND NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-010-04

PRIOR PLILAND DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

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APPLICANT: GU, Yizhong
APPLICANT: PRINK, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: GIANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ABONICANT
CURRENT APPLICATION NUMBER: US/09/866,108A
          PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
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Best Local Similarity 81.2%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches
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; Sequence 9915, Application US/09866108A
; Patent No. 6686188
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CORGANISM: Homo sapiens
US-09-866-108A-9914
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CORGANISM: Homo sapiens
US-09-866-108A-9915
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Sequence 9914, Application US/09866108A

Sequence 9914, Application US/09866108A

Sequence 9914, Application US/09866108A

Sequence 9914, Application US/09866108A

Settle No. 6686188

APPLICANT: GL, Yizhong

APPLICANT: GL, Yizhong

APPLICANT: FRIN, Sharron G.

APPLICANT: HANZEL, David K.

APPLICANT: SHANNON, Mark

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: WOSSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667
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ADDRESSE:
ADDRESSE:
ADDRESSE:
B. I. DU PONT DE NEMOURS AND
ADDRESSE:
COMPANY
STREET:
CITY:
WILMINGTON
STATE:
DISHWARE
COUNTRY:
U.S.A.
ZIP:
19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE:
RING BARE: 28 NOVEMBER: 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REFERENCE/DOCKET NUMBER: BB-1064-A
TELERPHONE: 302-982-8112
TELERPHONE: 302-92-28112
TELERPHONE: 302-92-28112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 302-892-8112
TELERAX: 302-992-949
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGHH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPLOGY: linear
COSCULE TYPE: DNA (genomic)
US-08-849-021-31
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Matches 13; Conservative
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GRNERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Leo
APPLICANT: Beigelman, Leo
APPLICANT: Beaudiy, Amber
APPLICANT: Beaudiy, Amber
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, David
APPLICANT: Adamic, Jasenka
APPLICANT: Berner
APPLICANT: Berner
APPLICANT: Berner
APPLICANT: Berner
APPLICANTON NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
FRIOR FILING DATE: 1999-12-10
FRIOR APPLICATION NUMBER: US 09/186,675
FRIOR APPLICATION NUMBER: US 09/301,511
FRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SEQ ID NO 143
LENGTH: 15
LENGTH: 15
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                                                                                                                                                                Sequence 2, Application US/09176320;
Sequence 2, Application US/09176320;
Patent No. 6172281;
GENERAL INFORMATION:
APPLICANT: Van Mellaert, Herman
APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
APPLICANT: Van Rie, Jeroen
TITLE OF INVENTION: PERVENTION OF BT RESISTANCE DEVELOPMENT
FILE REFERENCE: 021865-052
CURRENT APPLICATION NUMBER: US/09/176,320;
CURRENT APPLICATION NUMBER: US/09/176,320;
CURRENT APPLICATION NUMBER: PCT/EP90/00905
BARLIER APPLICATION NUMBER: PCT/EP90/00905
BARLIER APPLICATION NUMBER: PCT/EP90/00905
BARLIER FILING DATE: 1998-05-31
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
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51.0%; Score 10.2; D

Best Local Similarity 80.0%; Pred. No. 22;

Matches 12; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 143, Application US/09474432B Patent No. 6528640 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
, ORGANISM: Bacillus thuringiensis
US-09-176-320-2
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3 GGACTCGCTGGC 14
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CORGANISM: Homo sapiens
US-09-474-432B-143
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US-09-474-432B-143
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LENGIH: 15
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Sequence SEOS. Application US/09371772B

Patent No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozywe Pharmaceuticals, Inc.

APPLICANT: Ribozywe Pharmaceuticals, Inc.

APPLICANT: Bayco, Pam

APPLICANT: Bayco, Dam

APPLICANT: Becobedo, Jaim

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Pactor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Pactor Receptor

TITLE OF INVENTION NUMBER: US/09/371,772B

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR PLING DATE: 1995-10-26

PRIOR PLING DATE: 1995-10-26

PRIOR PLING DATE: 1995-10-26

NUMBER OF SEO ID NOS: 14225

SOFTWARE: PatentIn version 3.0

SEOTWARE: PatentIn version 3.0

LENGTH: 15
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Patent No. 6333152

GENERAL INFORMATION:

APPLICANT: Kinzler, Kenneth

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

TITLE REPERENCE: 0100 7/4664 US/09/081,646

CURRENT APPLICATION NUMBER: 60/047,352

EARLIER RPLICATION NUMBER: 60/047,352

EARLIER APPLICATION NUMBER: 60/047,352

SARLIER PLING DATE: 1997-05-21

NUMBER OF SEQ ID NOS: 871

SOFTWARE FEASTER FILM DATE: 1997-05-21

NUMBER: 05 SEQ ID NOS: 871

SEQ ID NO 637
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                                                            Gaps
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Pred. No. 20;
); Mismatches 1; Indels
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Query Match 56.0%; Score 11.2; DB 1; Length 17; Best Local Similarity 81.2%; Pred. No. 16; Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 22;
0; Mismatches
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Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                1 ATGGACTCGCTGGCAC 16
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Best Local Similarity 91.7%;
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-09-371-772B-5820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
) ORGANISM: Homo sapiens
US-09-081-646-637
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Gaps
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Pred. No. 25;
2; Mismatches 0; Indels
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US-08-363-240A-23/C

US-08-363-240A-23/C

Sequence 23, Application US/08363240A

Patent No. 5705388

GENERAL INFORMATION:

APPLICANT: Coulture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: PREVENTION, INHIBITION C
TITLE OF INVENTION: PROGRESSION AND REGRESSI
TITLE OF INVENTION: PROGRESSION AND REGRESSI
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Said West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STRATE: California
COUNTRY: U.S.A.

ZIP: 90071
ZIP: 9
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INHIBITION OF
AND REGRESSION
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IEM COMPATIBLE
COMPUTER: IEM COMPATIBLE
COMPUTER: IEM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
PILING DATE: December 23, 1994
PRIOR APPLICATION NUMBER: US/08/363,240A
PRIOR APPLICATION NUMBER: 23, 1994
APPLICATION NUMBER: 23, 1994
APPLICATION NUMBER: 210/096
FILING DATE:
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEFAX: 67-3510
INFORMATION POR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
INFORMATION POR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S ACTCGCTGGC 14
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Reigelman, Leo
APPLICANT: Reigelman, Leo
APPLICANT: Reigelman, Leo
APPLICANT: Reagelman, Leo
APPLICANT: Rarpeisky, Alex
APPLICANT: Rarpeisky, Alex
APPLICANT: Seedler, Dave
APPLICANT: Baynen, WINGER: US/09/476,387
CURRENT FILING DATE: 1999-12-29
FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-14-04-28
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 1524
SOFTMARE: PATENTIN VERSION 3.0
SEQ ID NO 143
LENGTH: 15
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                                                              Indels
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Sequence 112. Application US/08353240A
Fatent No. 570538
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: Couture, Larry
APPLICANT: Bagaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PROGRESSION AND RECRESSION
TITLE OF INVENTION: PROGRESSION AND RECRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS: 1243
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STRAET: California
COUNTRY: US.A.
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                                Pred. No. 22;
2; Mismatches
                                                                                                                                                                                                                                                                                                    US-09-476-387-143
; Sequence 143, Application US/09476387
; Patent No. 6617438
                             Best Local Similarity 66.7%; Pr
Matches 10; Conservative 2;
                                                                                                                         2 TGGACTCGCTGGCAC 16
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-363-240A-132
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US-08-584-040-8489
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STREET: 63
STREET: Su
                                                                                                                                                       JS-09-436-518-3
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                                                                                                                                                                                                                                                                                                               DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nishimura, Osamu
APPLICANT: Suenaga, Masato
APPLICANT: Obmae, Hiroaki
APPLICANT: Tauji, Shinji
TITLE OF INVENTION: Method of Removing N-terminal
TITLE OF INVENTION: Method ine
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: Boston
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                         2; Indels
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ZIP: 02109
COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFTWARE: PRESENCE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,417B
FILING DATE: 10-JUN-1997
CLASSIFTCATION: 514
PRIOR APPLICATION NUMBER: US/08/872,417B
FILING APPLICATION NUMBER: US/08/872,417B
FILING APPLICATION NUMBER: 27,026
RESERENCE/DOCKET NUMBER: 27,026
RESERENCE/DOCKET NUMBER: 27,026
RESERENCE/DOCKET NUMBER: 37,026
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Query Match
Best Local Similarity 84.6%; Pred. No. 27;
Best Local II, Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                               Score 9.8; D
Pred. No. 27;
                         REFERENCE/DOCKET NUMBER: 210/096
TELECOMMULTOATION INFORMATION:
TELEFHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08872417B Patent No. 6066470
                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 15 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-872-417B-3
                                                                                                                                                                                                                                                linear
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TOPOLOGY:
US-08-363-240A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
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US-08-872-417B-3
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SERVINIA TROUGHING TO US (03436518

TITLE OF INVENTION NEEDS (03421,17)

PRIOR PRINCE THING DATE: 1997-06-10

PRIOR PRINCE THING DATE: 1997-06-10

PRIOR PRINCE THING DATE: 1997-06-11

TITLE OF INVENTION NEEDS (03421,17)

PRIOR PRINCE THING DATE: 1996-06-14

FROM PRINCE THING DATE: 1996-06-14

TO REAL THING DATE: 1996-14

TO REAL THI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew
APPLICANT: Hiatt, Andrew
APPLICANT: Hiatt, Andrew
APPLICANT: Hiatt, Andrew
APPLICANT: No.
ITILE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
TITLE OF INVENTION: ROLLING TEMPLATES
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
CORRESPONDENCE MEATTLIK
STREET: 600 South, Avenue West
CITY: Westfield
STREET: New Jersey
COUNTRY: USA
ZIP: 07090
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Pred. No. 30;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CORRENT SECTION: PC-DOS/MS-DOS
SOCTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,856
FILING DATE: 15.5EP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
REGISTATION NUMBER: 33,071
REGISTATION NUMBER: ROSE 3.0-057
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: 908-654-5060
APPLICANT: Dierce, Michael L.
APPLICANT: Chen, Zhidong
TITLE OF INVENTION: Directed Antisense Libraries
FILE REFERENCE: T6678.PCT.US
CURRENT APPLICATION NUMBER: US/09/647,344A
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/US99/06742
PRIOR FILING DATE: 1999-03-28
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 34
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.0%; Score 9; DB 1;
100.0%; Pred. No. 31;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-929-856-3
; Sequence 3, Application US/08929856
; Patent No. 6136568
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA;
CRGANISM: herpes simplex virus
US-09-647-344A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGACTCGCTGG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-929-856-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
APPLICANT: Berobedo, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Becobedo, Jaime
TITLE OF INVENTION: Mevels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION NUMBER: US 60/005,974
FRIOR FILING DATE: 1999-08-10
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PATOR PATOR APPLICATION NUMBER: US 60/005,974
SEQ ID NO 4143
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9.8; D
Pred. No. 27;
                                                                              APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WALDURG, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELECHONE: (213) 489-1600
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8489:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
US-09-371-772B-4143
Sequence 4143, Application US/09371772B
; Patent No. 6566127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGACTCGCTGG 13
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-4143
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APPLICANT: Miyada
APPLICANT: Miyada
APPLICANT: Hubbell,
APPLICANT: Podor, S
APPLICANT: Huang, X
APPLICANT: Libshutz
APPLICANT: Libshutz
APPLICANT: Libshutz
APPLICANT: Sheldon,
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Sequence 44, Application US/08574396
Patent No. 6001648
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hendry, Philip
APPLICANT: Hendry, Philip
APPLICANT: Lockett, Trevor
TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES
TITLE OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
COUNTRY: USA
ZIP: 07090
COUNTRY EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER:
MAPLICATION NUMBER: US/08/929,856
FILING DATE: 15-SEP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
REGISTRATION NUMBER: 33,071
REGISTRATION NUMBER: 33,071
REDECOMMUTICATION INFORMATION:
TELEPHONE: 908-654-5000
"TELEPHONE: 908-654-5000
"TELEPHONE: POR-654-7000
"TELEPHONE: POR-654
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STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ATGGACTCG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
: U.S.A.
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US-08-574-396-44/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-929-856-4
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APPLICANT: Miyada, Charles Garrett
APPLICANT: Miyada, Charles Garrett
APPLICANT: Mibbell, Earl A.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua C.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Libshutz, Robert J.
APPLICANT: Loban, Peter E.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Detecting Cystic Fibrosis
NUMBER OF SEQUENCES: 250
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 13;
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CITY: Sec.
STATE: Califol...
STATE: Califol...
COUNTRY: USA
ZIP: 94111
COUNTRY: USA
COUNTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,301B
FILING DATE: 10-OCT-1995
CLASSIFICATION 1078ER: US/08/510,521
FILING DATE: 02-AUG-1995
FILING DATE: 02-AUG-1995
FILING DATE: 02-AUG-1995
FILING DATE: 02-AUG-1995
FILING DATE: PCT/US94/12305
COMPUTER READABLE FURM:
MEDIUM TYPE: Floppy disk
CMROUTER: IBM PC compatible
COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/574,396
FILING DATE: US-DSC-1995
ATTOMNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REBRENCE/DOCKET NUMBER: 1012/47203-A
TELEPHONE: 212 278-0400
TELEPHONE: 212 391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.0%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
US-08-574-396-44
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Ribozyme or portion thereof
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
OTHER INFORMATION: portions thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jos-U8-778-794A-81/c

Sequence 81, Application US/08778794A

Patent No. 6309823

GENERAL INFORMATION:
APPLICANT: Miyeda, Charles Garrett
APPLICANT: Miyeda, Charles Garrett
APPLICANT: Chee, Mark
APPLICANT: Chee, Mark
APPLICANT: Hubbell, Earl A.
APPLICANT: Lightur, Robert J.
APPLICANT: Lightur, Robert J.
APPLICANT: Lobban, Peter B.
APPLICANT: Lobban, Beter B.
APPLICANT: Sheldon, Edward L.
APPLICANT: Morris, MacDonald S.
APPLICANT: Morris, MacDonald S.
APPLICANT: Morris, MacDonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes
TITLE OF INVENTION: Arrays of Nucleic Acid Probes
TITLE OF INVENTION: Arrays of Nucleic Acid Probes
TITLE OF INVENTION: For Analyzing Biotransformation Genes
NUMBER OF SEQUENCES: 156
CORRESCED ADDRESS:
ADDRESSE: Two Enhancadero Center, Eighth Floor
SITRE CANTER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13
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STATE: CA
COUNTRY: USA
ZIP: 94111-338 FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM DATE:
APPLICATION DATE:
APPLICATION DATE: 03-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/778,794A
FILING DATE: 03-JAN-1997
APPLICATION NUMBER: US 08/143,312
PILING DATE: 05-OCT-1993
APPLICATION NUMBER: US 08/284,064
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: US 08/544,381
FILING DATE: 10-OCT-1995
APTORNEY AGENT INFORMATION:
NUMBER: 10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
FILE REFERENCE: 47203bpctus
CURRENT APPLICATION NUMBER: US/08/973,568B
CURRENT FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
LENGTH: 13
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REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGGACTCGC 10
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US-08-778-794A-81/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 13;
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US-09-156-028B-14/c
US-09-156-028B-14/c

Sequence 14, Application US/09156828B

Patent No. 6238917
GENERAL INFORMATION:
APPLICANT: Hendry, Philip
APPLICANT: McCall, Maxine J.
TITLE OF INVENTION: ASYMMETRIC HAWMERHEAD RIBOZYMES
FILE REFERENCE: 505340pu
CURRENT APPLICATION NUMBER: US/09/156,828B
CURRENT FILING DATE: 1998-09-18
PRIOR PELLIG DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 13
                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,064
FILING DATE: 02-040G-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-067-1993
ATTORNEY/AGBWT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 018547-004130US
TELEFARATION NUMBER: 018547-004130US
TELEFARONE/DOCKET NUMBER: 01854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.0%; Score 9; DB 1; Best Local Similarity 100.0%; Pred. No. 34; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (oligonucleotide) US-08-544-381B-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Gaps

Gaps

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Indels

Length 13;

DB 1;

45.0%; Score 9; DB 1 100.0%; Pred. No. 34; tive 0; Mismatches

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TYPE: DNA
CRGANISM: Artificial Sequence
FATURE:
CTHEN INFORMATION: Description of Artificial Sequence: synthetic
US-09-306-653-30
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 60/084,509
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: 09/135,183
; EARLIER FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 30
; SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 9; Conservative
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Fatent No. 660026
Fatent No. Changiun
Fatencant Yu. Changiun
Fatencant Yu. Changiun
Fatencant No. Electronic Methods for the Detection of Analytes
Fatencant Patencant No. Electronic Methods for the Detection of Analytes
Fatencant Patencant No. 1200-1787/RMS
CURRENT FILING DATE: 1999-05-06
FARLIER APPLICATION NUMBER: 60/084,509
FARLIER PILING DATE: 1998-05-06
FARLIER FILING DATE: 1998-05-06
FARLIER FILING DATE: 1998-05-06
FARLIER FILING DATE: 1998-06-06
FARLIER FILING DATE: 1998-06-06
FARLIER FILING DATE: 1998-06-06
FARLIER PILING DATE: 1998-06-07
FARLIER PILING DATE: 1998-08-17
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| Batent No. 660026
| GENERAL INFORMATION:
| APPLICANT: Bamdad, Cynthia C. | APPLICANT: Yu, Changjun | TITLE OF INVENTION: Electronic Methods for the Detection of Analytes | TITLE OF INVENTION: ULilaing Monolayers | FILE REFERENCE: A66343-1/RFT/RMS | CURRENT APPLICATION NUMBER: US/09/306,653 | CURRENT FILING DATE: 1999-05-06 | EARLIER APPLICATION NUMBER: 60/084,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-306-653-28
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100.0%; Pred. No. 34;
tive 0; Mismatches
                  018547-015700US
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
         REPERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
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STRANDEDNESS: single
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US-09-306-653-30/c
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US-09-306-653-28/c
                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                       APPLICANT: Bandad, Cynthia C.
APPLICANT: Bandad, Cynthia C.
APPLICANT: Yu. Changjun
TITLE OF INVENTION: Electronic Methods for the Detection of Analytes
TITLE OF INVENTION: Electronic Methods for the Detection of Analytes
TITLE OF INVENTION: Electronic Methods for the Detection of Analytes
TITLE REFERENCE: A66343-1/RET/RMS
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: 60/084,509
EARLIER FILING DATE: 1998-05-06
EARLIER PILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 13
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US-09-306-653-36/c
) Sequence 36, Application US/09306653
) Patent No. 660026
) GENERAL INFORMATION:
) APPLICANT: Bamdad, Cynthia C.
) APPLICANT: Damdad, Cynthia C.
) TITLE OP INVENTION: Electronic Methods for the Detection of Analytes
) TITLE OP INVENTION: Utilizing Monolayers
) FILLE APPRENCE: A6343-1,RET/RMS
) CURRENT APPLICATION NUMBER: US/09/306,653
) CURRENT APPLICATION NUMBER: US/09/306,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-306-653-34
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
US-09-306-653-34/c
Sequence 34, Application US/09306653
Patent No. 6600026
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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RESULT 32
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Patent No. 6600026
GENERAL INFORMATION
APPLICANT: Bandad, Cynthia C.
APPLICANT: Yu, Changjun
TITLE OF INVENTION: Electronic Methods for the Detection of Analytes
TITLE OF INVENTION: Utilizing Monolayers
FILE REFERENCE: A66343-IKRT/RMS
CURRENT APPLICATION NUMBER: US/09/306,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-306-653-42
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          Length 13;
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
EARLIER APPLICATION NUMBER: 60/084,652
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 60/084,509
EARLIER FILING DATE: 1998-05-06
EARLIER PELING DATE: 1998-05-06
EARLIER FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 47
SEQ ID NOS: 47
SEQ ID NOS: 47
LENGTH: 13
                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                   1 ATGGACTCG 9
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US-09-306-653-44/c
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1 Sequence 39, Application US/09621275

2 Sequence 39, Application US/09621275

3 Patcett No. 6646150:

4 Patcett No. 6646150:

5 Patcett No. 6646150:

5 PALCANT: Blackburn, Gary

7 TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC

7 TITLE OF INVENTION: DETECTION

7 TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC

7 TITLE OF INVENTION: AMPLIFICATION

7 TITLE OF INVENTION: AMPLIFICATION

7 TITLE OF INVENTION: AMPRER: US/09/621,275

7 CURRENT FILING DATE: 1999-07-20

7 PRIOR PILING DATE: 1999-01-27

7 PRIOR PILING DATE: 1998-01-27

7 PRIOR PILING DATE: 1998-01-27

7 PRIOR PILING DATE: 1998-01-27

7 PRIOR PILING DATE: 1998-05-06

7 PRIOR PILING DATE: 1998-01-29

7 PRIOR PILING DATE: 1998-01-29
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-306-653-44
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85.0%; Score 9; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: 60/084,652
EARLIER PILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 60/084,509
EARLIER PILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGACTCG 9
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 13
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APPLICANT: Blackburn, Gary
ITILE OF INVENTION: APPLICATION OF NUCLEIC ACIDS WITH ELECTRONIC
ITILE OF INVENTION: DETECTION
FILE REFERENCE: A-67643-2/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/621,275
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 09/134,698
PRIOR PILING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-27
PRIOR PLING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: 09/014,034
PRIOR PLING DATE: 1999-01-77
PRIOR PRIOR DATE: 1999-01-77
PRIOR PRIOR DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-16
PRIOR PRIOR DATE: 1999-06-06
PRIOR APPLICATION NUMBER: 60,084,509
PRIOR PILING DATE: 1999-05-06
PRIOR PELING DATE: 1999-06-06
                                                                                                                    JEGNERAL INFOGRATION:

JEGNERAL INFOGRATION:

JILLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC

TITLE OF INVENTION: DETECTION

FILE REPERBNCE: A-67643-27FT/RMS/RWK

CURRENT FILING DATE: 1099-07-20

PRIOR APPLICATION NUMBER: 06/144,698

PRIOR PLING DATE: 1999-01-27

PRIOR PLING DATE: 1999-01-27

PRIOR PLING DATE: 1999-01-27

PRIOR PLING DATE: 1999-01-27

PRIOR PLING DATE: 1998-01-27

PRIOR PLING DATE: 1998-06-06

PRIOR PLING DATE: 1998-05-06

PRIOR PLING DATE: 1998-01-29

PRIOR PLING DATE: 1998-01-29

PRIOR PLING DATE: 1998-01-29
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
                                  Sequence 41, Application US/09621275
Patent No. 6686150
GENERAL INFORMATION:
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US-09-621-275-45/c
; Sequence 45, Application US/09621275
; Patent No. 6686150
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41
LENGTH: 13
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US-US-621-2')-5-4')C

Sequence No. 6686150

Fatent No. 6686150

GENERAL INFORMATION:

APPLICANT: Blackburn Gary

TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC

TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS WITH ELECTRONIC

TITLE OF INVENTION: AMPLIFICATION NUMBER: 08/09/621,275

CURRENT APPLICATION NUMBER: 08/09/621,275

CURRENT APPLICATION NUMBER: 09/0144,698

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 09/014,034

PRIOR FILING DATE: 1998-08-07

PRIOR PLING DATE: 1998-08-07

PRIOR PLING DATE: 1998-08-06

PRIOR FILING DATE: 1998-06-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-07

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-07

PRIOR FILING DATE: 
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Batent No. 686550
Batent No. 686560
Batent No. 686560
Batent No. 98750
Batent No. 1000
BATION: APPLICANT: Blackburn, Gary
TITLE OF INVENTION: APPLICATION OF NUCLEIC ACIDS WITH ELECTRONIC TITLE OF INVENTION: DETECTION
FILE REFERENCE: A-67643-2/RFT/RMS/RMK
                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: synthetic. US-09-621-275-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), OTHER INFORMATION: Description of Artificial Sequence: synthetic.
US-09-621-275-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                     Length 13;
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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45.0%; Score 9; DB 1
100.0%; Pred. No. 34;
Live 0; Mismatches
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                             Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 ACTCGCTGGCAC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
                                                                                                                                                                                                             10 ATGGACTCG
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US-08-547-214-19
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US-08-547-214-20
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GENERAL INFORMATION:
APPLICANT: Blackburn, Gary
TITLE OF INVENTION: APPLICATION OF NUCLEIC ACIDS WITH ELECTRONIC
TITLE OF INVENTION: APPLICATION NUMBER: US/09/621,275
CURRENT APPLICATION NUMBER: US/09/621,275
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 00/144,698
PRIOR APPLICATION NUMBER: 00/144,698
PRIOR APPLICATION NUMBER: 00/124, 34
PRIOR PILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 09/236,351
PRIOR APPLICATION NUMBER: 09/135,183
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/084,425
PRIOR APPLICATION NUMBER: 60/084,425
PRIOR APPLICATION NUMBER: 60/084,509
PRIOR APPLICATION NUMBER: 60/084,509
PRIOR APPLICATION NUMBER: 60/084,509
PRIOR APPLICATION NUMBER: 60/084,509
PRIOR PILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1996-10-09
PRIOR FILING DATE: 1996-10-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/621,275
CURRENT FILING DATE: 2002-02-12
                CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/144,698
PRIOR APPLICATION NUMBER: 60/144,698
PRIOR PILING DATE: 1999-07-20
PRIOR PLING DATE: 1999-07-20
PRIOR PELING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-27
PRIOR FILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/084,425
PRIOR APPLICATION NUMBER: 60/084,425
PRIOR PLING DATE: 1998-06-06
PRIOR PLING DATE: 1998-06-06
PRIOR PLING DATE: 1998-05-06
PRIOR PLING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 78
SOFTWARE PRECENTING VOTE: 2.1
SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i-09-621-275-55/c
Sequence 55, Application US/09621275
Patent No. 6686150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/08547214
Patent No. 5871697
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: Simpson, John
TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 34;
0; Mismatches 2; Indels
                                                              0; Indels
Length 13;
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Patent No. 5871697
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: Deem, Michael
APPLICANT: Simpson, John
TITLE OF INVENTION: Method for the Determination and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDKESSE: Pennie and Edmonds
STREET: New York
CITY: New York
CITY: New York
CUTYRR: New York
CUTYRR: New York
CUTYRR: NGA 2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/547,214
FILING DATE: 24-OCT-1995
CLASSIFICATION NUMBER: US/08/547,214
FILING DATE: 24-OCT-1995
CLASSIFICATION: NOMBER: 1995
TELECOMMUNICATION INFORMATION:
NAME: MASTOCK, S. LEGILE
REGISTRATION NUMBER: 1987
TELEPAN: (212)-790-900
TELEFAX: (212)-790-900
TELEFAX: (212)-790-900
TELEFAX: (212)-790-900
TELEFAX: (212)-790-900
TELEFAX: (212)-869-8864
TELEFAX: (212)-899-815
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TTORNEY/AGENT INFORMATION:
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Best Local Similarity
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US-08-663-823B-20
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APPLICANT: Rothberg, Jonathan
APPLICANT: Rothberg, Jonathan
APPLICANT: Rothberg, John
TITLE OF INVENTION: METHOD AND APPARATUS FOR IDENTIFYING,
TITLE OF INVENTION: WITHOUT SEQUENCING
TITLE OF INVENTION: WITHOUT SEQUENCING
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie and Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without TITLE OF INVENTION: Sequencing NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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                                                        COMPRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
CITY: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 1036-2711
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Petentin Release #1.0, Version #1.30
SOFTWARE: Petentin Release #1.0, Version #1.30
CUMERNY APPLICATION DATA:
APPLICATION DATA: 24-007-1995
CLASSIFTCATION NUMBER: 18,872
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE DOCKET NUMBER: 7934-015-999
TELEPHONE: (212)-790-9090
TELEPHONE: (212)-790-9090
TELEPHONE: (212)-790-9090
TELEPHONE: (212)-869-8864
TELEPHONE: (212)-869-8864
TELEPHONE: LENGTH: 12 base pairs
TERMINE MISSIFTCE:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT READBLE FORM:
COMPUTER. READBLE FORM:
MEDIUM TYPE:
COMPUTER. IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBERS: US/08/663,823B
FILING DATE: 14.7une-1996
CLASSIFICATION: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 8.8; DB
Pred. No. 34;
0; Mismatches
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EET: Pennie and Edmonds LLP
EET: 1155 Avenue of the Americas
T.: New York
TY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/08663823B Patent No. 5972693
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 ACTCGCTGGCAC 16
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US-08-942-406-18
Sequence 10, Application US/08942406
Patent No. 6141657
GENERAL INFORMATION:
Simpson, John
TITLE OF INVENTION: Method for the Determination and NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER: READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTI Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/942,406
FILING DATE: OL-CC-1997
CLASSIFICATION NUMBER: 08/547,214
FILING DATE: CUNKNOWN>
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 189.97
TELEPROMEDIES: 1212)-190-9090
TELEPRAN: (212)-190-9090
TELEPRAN: (212)-190-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8.8; DB 1; Length 12;
Pred. No. 34;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08942406
Patent No. 6141657
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
Deem, Michael
Simpson, John
TITLE OF INVENTION: Method for the Determination and
NUMBER OF SEQUENCES: 59
 7
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66441 PENNIE INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 10; Conservative
10; Conservative
                                 5 ACTCGCTGGCAC 16
                                                                 1 AGTCGCTGGCGC 12
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                                                                                                                      RESULT 41
US-08-942-406-18
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US-08-942-406-20
Matches
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OURRESPONDERS: Pennie and Educade

JUNDESSESS: Pennie and Educade

GTITE: New York

GTITE: New York

GTITE: New York

GONFILE: Under County: U
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TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
CHER INFORMATION: Primer
US-09-203-231B-22
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Best Local Similarity 83.3%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                              44.0%;
                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3
Matches 10, Conservative
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COTHER INFORMATION: Primer
US-09-203-231B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ACTCGCTGGCAC 16
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; STRANDEDNESS: single ; TOPPLOGY: linear ; MOLECULE TYPE: DNA US-09-322-617-20
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US-09-203-231B-24
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US-09-203-231B-22
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| Patent No. 6211812
| GENERAL INFORMATION:
| APPLICANT: Rothberg, Jonathan | APPLICANT: Deem, Michael | APPLICANT: Deem, Michael | APPLICANT: Deem, Michael | APPLICANT: Simpson, John for the Determination and | TITLE OF INVENTION: Guencing | TITLE OF INVENTION: Guencing | VIVENTION: Sequencing | VIVENTION: VIVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FOR:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-SOFTWARE: PATENTIN NUMBER: US/09/322,617
FILING DATE:
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 18,872
REJEFFICH (212)-699-864
TELEFFICH (212)-699-864
TELEFFICH (212)-699-864
TELEFFICH (212)-699-864
TELEFFICH (212)-699-864
TELEFFICH (212)-69-864
                             PULGASJITION DATA:
PULGATION DATA:
APPLICATION NUMBER: 08/547,214
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 18,872
RELECHANCATION INFORMATION:
TELECHANCATION INFORMATION:
TELETAX: (212)-869-8864
TELETAX: (212)-869-8864
TELETAX: (212)-869-8864
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: NUCLEIC acid
STRANDEDNESS: single
MULBCULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ACTCGCTGGCAC 16
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US-09-322-617-20
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Score 8.8; DB 1; Length 12;
Pred. No. 34;
0; Mismatches 2; Indels
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Pred. No. 34;
0; Mismatches 2; Indels
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| Sequence 24, Application US/09203231B
| Patent No. 6355423
| GENERAL INFORMATION:
| APPLICANT: Rothberg, Jonathan M
| APPLICANT: Rothberg, Jonathan M
| APPLICANT: Hu, Xinghua |
| TITLE OF INVENTION: Differential Gene Expression |
| TITLE OF INVENTION: Differential Gene Expression |
| FILE REFERENCE: 7934-052 |
| CURRENT APPLICATION NUMBER: US/09/203,231B |
| CURRENT APPLICATION NUMBER: 60/105,305 |
| PRIOR PILING DATE: 1997-12-03 |
| NUMBER OF SEQ ID NOS: 88 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH 122 |
| LENGTH 123 |
| LENGTH 123 |
| LENGTH 124 |
| LENGTH 124 |
| LENGTH 125 |
| LENGTH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yequence 22, Application US/09203231B
patent No. 635643
papellCant: Noallur, Girish N
papellCant: Noallur, Girish N
papellCant: Noallur, Girish N
proceed Noallur, Girish N
papellCant: Do. 10062
proceed Noallur, Girish N
proceed Noallur, Noallur, Noallur, Soluting Nate: 1997-12-03
proceed Noallur, Noallur, Noallur, Soluting Nate: 1997-12-03
proceed Noallur, Noallur, Noallur, Soluting Nate: 1997-12-03
proceed Noallur, Noal
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                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: Deem, Michael
APPLICANT: Simpson, John
TITLE OF INVENTION: Method for the Determination and
TITLE OF INVENTION: Olassification of DNA Sequences in a Sample Without
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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  Length 12;
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                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPOTER: EN PC Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,561
FILING DATE:
PILING APPLICATION DATA:
APPLICATION NUMBER: 08/547,214
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 18,872
REFERENCE/POCKET NUMBER: 18,872
REFERENCE/POCKET NUMBER: 18,872
RELEPHONE: (212)-790-9090
TELEFPK: (212)-790-9090
  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8.8; DB
Pred. No. 34;
0; Mismatches
Score 8.8; DB Pred. No. 34; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 48
US-09-751-561-20
; Sequence 20, Application US/09751561
; Patent No. 6418382
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
; APPLICANT: Deem, Michael
                                                                                                                                                                        RESULT 47
US-09-751-561-18
; Sequence 18, Application US/09751561
; Patent No. 6418382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%;
ilarity 83.3%;
Conservative
Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                             S ACTCGCTGGCAC 16
                                                                                                                    1 AGTCGCTGGCGC 12
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: DNA
US-09-751-561-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
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Matches
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  John
Method for the Determination and
Classification of DNA Sequences in a Sample Without
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Pred. No. 34;
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TITLE OF INVENTION: Method for the Determination and NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: USA
ZIP: 10136-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,561
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leblie
REGISTATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 7934-015-999
TELERRAXI (212)-790-9090
TELERRAXI (212)-790-9090
TELERRAXI (212)-790-9090
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
APPLICANT: Simpson, John
TITLE OF INVENTION: Method for the Deter
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 49
US-09-724-385-18
US-09-724-385-18
Sequence 18, Application US/09724385
Patent No. 643281
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rothberg, Jonathan
Deem, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)-869-886-
TELEX: 6641 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHRACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGTCGCTGGCGC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                   CITY: Nev
STATE: Ne
COUNTRY:
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RESULT 52
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/724,385

FILING DATE: 28-No. 6432361-2000

CLASSIFICATION: CURROWN>

PRIOR APPLICATION NUMBER: 09/322,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8.8; DB 1; Length 12;
Pred. No. 34;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09724385

Patent No. 6432361

GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
Deem, Michael
Simpson, John
TITLE OF INVENTION: Method for the Determination and
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/09/724,385
FILING DATE: 28-No. 6432561-2000
CLASSIFICATION: -Unknown>
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: -UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,972
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/COCKET NUMBER: 7934-015-999
TELECOMOUNICATION INFORMATION:
TELEPHONE: (212)-790-9090
TELEFAX: (212)-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
TOPOLOGY: linear
;
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-724-385-18
                                                                                                                                                                                                                                                                                                         TELEFAX: (212)-869-886
TELEX: 6641 PENNIE
INFORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66441 PENNIE INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: USA
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US-09-724-385-20
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/757,528
FILING DATE: 10-Jan-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION: CURROWN>
PRIOR APPLICATION NUMBER: 08/547,214
FILING DATE: CURROWN>
APPLICATION NUMBER: 08/547,214
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
REGISTRATION NUMBER: 18/87
REDERENCE/DOCKET NUMBER: 7934-015-999
TELECOMPUNICATION INFORMATION:
                                                                                                                                                   Score 8.8; DB 1; Length 12;
Pred. No. 34;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, John
TITLE OF INVENTION: Method for the Determination and
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8.8; DB 1;
Pred. No. 34;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-757-528-18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-724-385-20
                                                                                                                                                                                                                                                                                                                                                           RESULT 31
US-09-775-528-18
Sequence 18, Application US/09757528
; Patent No. 6453245
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
APPLICANT: Rothberg, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)-86-98-4
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   44.0%;
Best Local Similarity 83.3%;
Matches 10; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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Patent No. 5882914
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Joila
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           Sequence 20, Application US/09757528
Fatent No. 6453245
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
Beem, Michael
Slumpson, John
TITLE OF INVENTION: Method for the Determination and
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie and Edmonds
STRREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                            STATE: New York
CUIT: New York
ZIP: 10036-2711
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/757,528
FILING DATE: 10-7an-2001
CLASSIFICATION SOFTEM: 06/47,214
APPLICATION NUMBER: 08/547,214
APPLICATION NUMBER: 08/547,214
ATTORNEY/AGENT INFORMATION:
NAME: MISCOCK, S. Leelie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-015-999
TELEFAAT: ON INFORMATION:
TELEFAAT: ON INFORMATION:
TELEFAAX: (212)-790-9090
TELEFAAX: (212)-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 34; tive 0; Mismatches 2; Indels
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MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-757-528-20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 ACTCGCTGGCAC 16
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STATE: CA
COUNTRY:
US-09-757-528-20
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CURRENTING PRICE TO CONTROL TO A STEER NEW TO A VERSION #1.30

PELLICATION NUMBER: US/08/480.473B

PELLICATION NUMBER: US/08/480.473B

PELLICATION NUMBER: US/08/480.473B

PELLICATION NUMBER: US/08/480.473B

PELLICATION NUMBER: US/08/58/58101

PERSENCE/COCKET NUMBER: 18,347

PERSENCE/CO
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                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09235217
Patent No. 6222018
GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
COMMERS PONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
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                                                                                       ;; Score 8.2; DB 1; Length 12;
;; Pred. No. 46;
12; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Fatentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,217
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILENCY CATES

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEFAX: 619/678-5070
TELEFAX: 619/678-5090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: N is inosine. Us-09-235-217-25
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: N is inosine.
US-08-915-213-25
                                                                                         Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative 7
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Best Local Similarity 70.0'
Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 TGGCACGCAC 20
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12 TSKCACGCNC 3
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                                                                                                                                                                                                                                                         RESULT 55
US-09-235-217-25/c
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RESULT 56
PCT-US96-10251-25/c
; Sequence 25, Application PC/TUS9610251
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine

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TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolia
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPTTER: END PC COMPATION:
MEDIUM TYPE: Floppy disk
COMPUTER: END PC COMPATION:
OURRENT APPLICATION TO PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PCT/US96/10251
FILING DATE: 06-UTN-1996
CLASSIFICATION:
COMPATION:

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Sequence 179, Application US/08859954
Patent No. 6083655
Patent No. 6083655
GENERAL INPORMATION; Susan H.
APPLICANT: Hardin, Paul B.
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER: FRADABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: US-SECONDENCE NOTA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: N is inosine. PCT-US96-10251-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Haile, Liga A.
REGISTRATION NUMBER: 38,347
REFRENCE/DOCKET NUMBER: 07265
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.0%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 TGGCACGCAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 TSKCACGCNC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-859-954-179/c
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HYPOTHETICAL: NO ; ANTI-SENBE: NO US-08-351-748-13
                                                                                                                                                           7 TCGCTGGC 14
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US-08-351-748-13/c
US-08-171-385-28
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40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 58
US-08-171-385-28/C
| Sequence 28, Application US/08171385
| Patent No. 552784
| GENERAL INFORMATION:
| APPLICANT: Mary E. Russell
| APPLICANT: Ulrike Utans
| TITLE OF INVENTION: Mediators of Chronic Allograft
| TITLE OF INVENTION: ARejection NUMBER: Signal Allograft
| TITLE OF INVENTION: ABSOLUTION OF STATE: Massachusetts
| CONTUREX: Boston STATE: Massachusetts | STATE: Massachusetts | STATE: COMPUTER: IBM PS/2 Model 502 or 553X |
| COMPUTER: IBM PS/2 Model 502 or 553X |
| COMPUTER: IBM PS/2 Model 502 or 553X |
| COMPUTER: IBM PS/2 Model 502 or 553X |
| COMPUTER: IBM PS/2 Model 502 or 553X |
| COMPUTER: Wordberfect (Version 5.1) |
| CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/171,385 |
| FILING DATE: FILING DATE: PILING DATE: PILING DATE: PILING DATE: PILING DATE: PILING DATE: PILING DATE: APPLICATION NUMBER: 34,819 |
| REFERENCE/DOCKET NUMBER: 34,819 |
| REFERENCE/DOCKET NUMBER: 34,819 |
| REFERENCE/DOCKET NUMBER: GA433/006001 |
| TELESPHONE: G17) 542-8906 |
| TELESPHONE: G17) 542-8906
                    FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REGISTRATION NUMBER: 32,714
REGISTRATION NUMBER: 13,714
TELEPHONE: 713/61-5325
TELEPHONE: 713/61-5325
TELEPHONE: 713/61-5325
TELEPHONE: 713/61-5325
TELEPHONE: 713/61-5325
TELEPHONE: 713/61-5325
TELEPHONE: 713/61-5246
TELEPHONE: 713/61-5246
TELEPHONE: 713/61-5246
TELEPHONE: 110/61
SEQUENCE CHARACTERITICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 110/61
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "olgionucleotide"
HYPOTHETICAL: YES
MIT -SENSE: YES
US-08-859-954-179
APPLICATION NUMBER: 08/632,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TYPE:
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STRANDEDNESS: single
TOPOLOGY: linear
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| Query Match
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REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 2888-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 14:
INFORMATION FOR SEQ ID NO: LEIEX: 106141
INFORMATION FOR SEQ ID NO: LEIEX: LEIGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERASTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TCGCTGGC 14
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                                                                                                                                                                                                                                                                                                                                                                            linear
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TOPOLOGY:
US-08-463-660-14
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US-08-463-660-14/C
Sequence 14, Application US/08463660
Sequence 14, Application US/08463660
Sequence 14, Application US/08463660
GENERAL INFORMATION:
APPLICANT: SMITH, HELENE S.
APPLICANT: SMITH, LING-CHUN
TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND TREATMENT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
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                                          ISOLATING, AND CLONING
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                                                                                                                                                                                                                                                         COUNTY: BOSCON

COUNTY: BOSCON

ZATA: MA

COUNTRY: USA

CONPUTER: ELSDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
CORPOTER: TEM PC compatible
CORPOTER: TEM PC COMPATION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,536A
FILING DATE: 25-APR-1995
CLASSIFICATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 181411-012
TELEFRAX: (617) 248-4000
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CITY: Palo Alto
COUNTR: California
COUNTR: California
COUNTR: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: EN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,660
                                                                                                       NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART
STREET: 53 State Street
CITY: Boston
          APPLICANT: Pardee, Arthur B.
TITLE OF INVENTION: IDENTIFYING, II
TITLE OF INVENTION: MESSENGER RNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; P
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ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TCGCTGGC 14
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Best Local Similarity
Matches 8; Conserv
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| Patent No. 5776633
| GENERAL INFORMATION:
APPLICANT: SMITH, HELENE S.
| APPLICANT: CHUN, LING-CHEN.
| TITLE OF INVENTION: TREGETS FOR BREAST CANCER DIAGNOSIS AND TITLE OF INVENTION: TREATMENT |
| NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESSE: MORRISON & FOERSTER |
| STREET: 755 Page Mill Road |
| CITY: Palo Alto |
| STATE California
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Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 94304-1018

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION PATA:
APPLICATION NUMBER: US/08/678,280
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REFERENCZ/DOCKET NUMBER: 2888-20001.20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
Query Match

40.0%; Score 8; DB 1.
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.0%; Score 8; DB 1
100.0%; Pred. No. 41;
Live 0; Mismatches
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PatentIn Release #1.0, Version #1.30
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SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
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TELEX:
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US-08-684-547-13/C
US-08-684-547-13/C
Sequence 13 Application US/08684547
Patent No. 5965409
GENERAL INFORMATION:
APPLICANT: Pardee Ph.D., Arthur B.
APPLICANT: Liang Ph.D., Peng
APPLICANT: Pe
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40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/582,261A

FILING DATE: 03-JAN-1996

CLASSIFICATION: 435

ATTORNEY/AGRAT INPORMATION:

NAME: Heslin, James M.

REFERENCE/DOCKET NUMBER: 016558-001200US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELETHORE: 415-576-0300

INPORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: ALCOPLOKE SINGLE
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COUNTRY: USA
ZIP. 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,819
FILING DATE: 02-0CT-1997
CLASSIFICATION NUMBER: 60/058,520
FILING DATE: 11-SEP-1997
ATTOMNEY/AGENT INFORMATION:
NAME: Granahan, Particia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BIH96-13pA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEDENOWS: 781-861-6240
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,547
FILING DATE: 19-UUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JAITELL Ph.D., Brenda H.
REGLSTRATION NUMBER: 39,223
REPRENGE/DOCKET NUMBER: 0181411-0013
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 248-5000
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
LEMOTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: Incert
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US-09-016-540-4
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US-08-361-441B-28/C
| Sequence 29, Application US/08361441B
| Sequence No. 6077948
| GENERAL INFORMATION:
| APPLICANT: Ususell Mary E. APPLICANT: Ususell Nary E. AUDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
| CITY: Boston Nary E. AUDRESSEE: MA. AUDRESSEE:
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ZIP: 02110-2804

ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskett
                                                                                                                                                                                                                                                                                                              40.0%; Score 8; DB 1
100.0%; Pred. No. 41;
tive 0; Mismatches
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40.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches
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Patent No. 6132965
GENERAL INFORMATION:
APPLICANT: Austin, Richard C.
APPLICANT: Hirsh, Jack
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-942-819-3
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
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US-09-016-540-4/c
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APPLICANT: Weitz, Jeff
TITLE OF INVENTION: Methods and Compositions for Diagnosis
TITLE OF INVENTION: of Hyperhomocysteinemia
NUMBER OF SEQUENCES: 9
CARRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
STREET: Two Embarcadero Center, 8th Ploor
STREET: CA
STREET: CA
STREET: CA
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ORGANISM: Artificial Sequence
FEATURE:
OCHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-55
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Satent No. 6284466
GERREAL INFORMATION:
APPLICANT:
BERSON. HIGH RESOLUTION GENOME SCANNING
FILE REPERBENCE:
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 10
                                                                                                                                                                                                                           ZIF: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,540
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.0%; Score 8; DB 1; Best Local Similarity 100.0%; Pred. No. 41; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/582,261
FILING DATE: 03-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFRENCE/DOCKET NUMBER: 0165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFRAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 TCGCTGGC 14
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US-09-398-499-55/c
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Gaps
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                APPLICANT: Gall, MINING
TITLE OF INVENTION: RINZ, A NOVEL INHIBITOR OF RAS-MEDICATED
TITLE OF INVENTION: RINZ, A NOVEL INHIBITOR OF RAS-MEDICATED
TITLE OF INVENTION: RINZ, A NOVEL
TITLE OF INVENTION: SIGNALING
FILE REFERENCE: 1440-1089-004
CURRENT APPLICATION NUMBER: US/09/522,955A
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: PCT/US98/19056
PRIOR APPLICATION NUMBER: US 08/942,819
PRIOR PILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-09-11
PRIOR FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FABELSEQ for Windows Version 4.0
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application PC/TUS9302246
Sequence 13, Application PC/TUS9302246
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lang, Peng
APPLICANT: Pardee, Arthur B.
TITLE OF INVENTION: Identifying, Isolating and Cloning
TITLE OF INVENTION: Messenger RNAs
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 21
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: Choate, Hall & Stewart
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUDERSOBE: CHORDE, MAIL & SLEWALL
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02190
COMPUTER: Exchange Place, 53 State Street
ZIP: 02190
COMPUTER: ELOPDY disk
COMPUTER: ELOPDY disk
COMPUTER: IBM PC COMPATIBLE
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02246
FILING DATE: 19330311
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/850,343
FILING DATE: 11-MAR-1992
ATTONEY/AGENT INPORMATION:
NAME: PASTERNOR/DOCKET NUMBER: 29,576
REGERRATION NUMBER: 29,576
REGERRATION NUMBER: 29,576
REFERENCE/COMPUTION: TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-522-955A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617 227-5020
TELEPAX: 617 227-5020
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TCGCTGGC 14
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                                                                                                                     RESULT 69
US-09-308-984-3/C
| Sequence 3, Application US/09308984
| Sequence 3, Application US/09308984
| Patent No. 6388065
| CENERAL INFORMATION:
| APPLICANT: Durek, Matthias
| APPLICANT: Durek, Matthias
| TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
| FILLE REFERENCE: SCHU 204 (09902857)
| FILLE REFERENCE: SCHU 204 (09902857)
| PRIOR PELICATION NUMBER: PCT/DE97/02660
| PRIOR PILLING DATE: 1996-11-12
| PRIOR PPLICATION NUMBER: DE 196 49207
| PRIOR PILLING DATE: 1997-11-27
| PRIOR PILLING DATE: 1997-11-27
| SEQ ID NO 3
| LEGITH 10
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US-09-313-221A-132/c
; Sequence 132, Application US/09313221A
; Patent No. 6468743
; GENERAL INFORMATION:
; APPLICANT: Thomas L. Romick (Inventor)
; TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
; TITLE OF INVENTION: POR TECHNIQUES FOR DETECTING MICROBIAL
; TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS
; TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS
; TITLE OF INVENTION: DATE: 1999-05-17
; PRIOR PELLING DATE: 1999-05-18
; SOFTWARE: FESTERE 1 1998-05-18
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastESEQ for Windows Version 4.0
; SEQ ID NO 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Pred. No. 41;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels
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| Sequence 3, Application US/09522955A
| Patent No. 6509942
| GENERAL INFORMATION:
| APPLICANT: Tam, See-Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Compylobacter jejuni
US-09-313-221A-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%;
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Best Local Similarity 100.
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-09-308-984-3
CGCTGGCA 15
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                                                  CGCTGGCA 2
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APPLICANT: Wang, Churvei
APPLICANT: Wang, Churvei
APPLICANT: Jenhart, Derek H.
APPLICANT: Lipphutz, Robert J.
APPLICANT: Lipphutz, Robert J.
TITLE OF INVENTION: Computer-Aided Visualization and
TITLE OF INVENTION: Analysis System for Sequence Evaluation
Fatent No. 5795716
MUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,525A
FILING DATE: October 21, 1994
CLASSIFICATION: 435
                                                                                                          40.0%; Score 8; DB 1;
100.0%; Pred. No. 41;
tive 0; Mismatches
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: No. 5795716viel, Vernon A.
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528X-82
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      RESULT 73
US-08-327-525A-39
US-08-327-525A-39
Sequence 39, Application US/08327525A
Setent No. 5795716
GENERAL INFORMATION:
; MOLECULE TYPE: other nucleic acid
; HYPOTHEITOL: NO
; ANTI-SENSE: NO
PCT-US93-02246-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                          Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 CTGGCACG 17
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RESULT 74 18-08-51-31-378-39 ; Sequence 39, Application US/08531137B ; Patent No. 5974164

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GENERAL INFORMATION:

TITLE OFFINDENTION:

ATTHE OFFINDENTION Computer-Aided Vanalisation and
TITLE OFFINDENTION Computer-Aided Vanalisation and
TITLE OFFINDENTION COMPUTER.

MANAGERS OFFINDENTIAN COMPUTER.

TOTAL A Lea Camino Real, Site 265

COMMENTE CALIFORM A Lea Camino Real, Site 265

CONTRICT: CALIFORM A Lea Camino Real, Site 265

CONTRICT CALIFORM A LEA CALIFORM A LEA CALIFORM A LIGHT A LEA CALIFORM A LIGHT A
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RESULT 78
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Fatent No. 6607887
GENERAL INPORMANTION.
TITLE OF INVENTION: Computer-Aided Visualization and
Analysis System for Sequence Evaluation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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US-09-249-155A-312/C

| Sequence 312, Application US/09249155A
| Patent No. 6588173
| GENERAL INFORMATION:
| APPLICANT: Heber-Katz, Ellen
| TITLE OF INVENTION: Compositions and Methods for Wound
| TITLE OF INVENTION: Healing
| FILE REFRENCE: 00466.78503
| CURRENT APPLICATION NUMBER: US/09/249,155A
| CURRENT FILING DATE: 1999-02-12
| PRIOR APPLICATION NUMBER: US 60/097,937
| PRIOR PILING DATE: 1998-02-13
| PRIOR PILING DATE: 1998-02-13
| PRIOR FILING DATE: 1998-09-26
| PRIOR FILING DATE: 1998-09-26
| WUMBER OF SEC ID NOS: 346
| SOFTWARE: FastSEC for Windows Version 4.0
| LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/531,137
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ritter, Michael J.
REGISTRATION NUMBER: 36,653
REFERENCE/DOCKET NUMBER: AFFYPOO6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-903-3500
TELEFAX: 650-903-3501
INFORMATION FOR SEQ ID NO: 39:
BENCHANCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
US-09-158-765-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 6607887
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 CTGGCACG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 GGCACGCA 19
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US-09-796-071-39
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TTREET: 4906 ED Camino Real, Suite 205

CITY 1.00 ALTON

CONFITES TABLOADE FORM:

CONFITES TRADAGLE FORM:

FILING DATE: JT-F60-1001

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION THOMBOWATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 hear pairs

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 hear pairs

ON 1 CTGCCAGG 9

DOMESTICATION SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 hear pairs

ON 1 CTGCCAGG 9

SEQUENCE CHARACTERISTICS:

ADDRESSES MARNILLA:

APPLICANT: Hart, Andrew

APPLICANT: Hart, Andrew

APPLICANT: Hart, Andrew

APPLICANT: Hart, Andrew

APPLICANT: HEART, ANDREW

APPLICANT: HEART, ANDREW

ANDRESSES: MARNILLS:

ADDRESSES: MARNILLS:

MADING THE CORPORED STRANE

SECUENCE CONFURENTION:

MADING CORPUSED STRANE

POWER THE PROPERTY OF A CONFURENTION:

MADING CORPUSED TRANES FORM:

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; Sequence 4, Application US/08152955
; Patent No. 5474897
; GENERAL INFORMATION: Arthur
APPLICANT: Fraser, James
; TITLE OF INVENTION: Screening Assay for the Identification
; TITLE OF INVENTION: of Immunosuppressive Drugs
; CORRESPONDERS: 5
; CORRESPONDERS: Towneed and Townsend
; TREET: One Market Plaza, Steuart Tower, Suite 2000
; STREET: California
; STREE: California
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                                                                                                                                                                                                                                                                             Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: RIDAPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,955
PRIOR APPLICATION NUMBER: US 07/898,639
FILING DATE: 15-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               40.0%; Score 8; DB 1; 100.0%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.0%; Score 7.8; DB
81.8%; Pred. No. 50;
tive 0; Mismatches
REGISTRATION NUMBER: 33,071
REBERENCS/DOCKET NUMBER: ROSE 3.0-057
FILECOMMUNICALION INFORMATION:
TELEPHONE: 908-654-500
TELEPHONE: 908-654-7866
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNES; single
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFRENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8'
                                                                                                                                                                                                                                                                                                                      Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserval
                                                                                                                                                                                                                                                                                                                                                                                               5 Arddacrc 12
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                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA US-08-929-856-5
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US-08-152-955-4/c
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Gaps

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2; Indels

2 TGGACTCGCTG 12

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Sequence 78, Application US/08874825

Baten No. 6057101

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Rothberg, Jonathan

APPLICANT: Raight, James

APPLICANT: Kaight, James

APPLICANT: Kaight, James

APPLICANT: Kaight Theodore

TITLE OF INVENTION: IDRNTIFICATION AND COMPARISON OF

TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

SEQUENCES: 122

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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RESULT 80

PCT-10593-05668-4/C

Sequence 4, Application PC/TUS9305668

Sequence 4, Application PC/TUS9305668

Sequence 4, Application PC/TUS9305668

SENERAL INPORMATION:
APPLICANT: Weiss, Arthur
APPLICANT: Weiss, Arthur
TITLE OF INVENTION: Of Immunosuppressive Drugs
TITLE OF INVENTION: Of Immunosuppressive Drugs
NUMBER OF SEQUENCES:
ADDRESSEE: Fisher & Amzel
STREET: 1120 Harbor Bay Parkway, Suite 225
CITY: Alameda
STRTE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Elam PC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05668
FILING DATE: 19930611
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/898,639
FILING DATE: 15-UTW-1992
ATTORENYAGENT INFORMATION:
NAWE: Fisher, Stanley P.
REGISTRATION NUMBER: 24,344
REFRENCE/DOCKET UNMBER: 24,344
REFRENCE/DOCKET UNMBER: 91-143-1PCT
TELEPHONE: 510-748-6868
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENDTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7.8; DB Fred. No. 50; O; Mismatches
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
TOPOLOGY: linear
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2 TGGACTCGCTG 12
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US-08-874-825-79
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Sequence 79, Application US/08874825

Sequence 79, Application Manalanan

APPLICANT: Nandabalan Krishnan

APPLICANT: Raibfleisch, Theodore

ITILE OF INVENTION: DEDTIFICATION AND COMPARISON OF

ITILE OF INVENTION: PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS

ITILE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS

NUMBER OF SEQUENCES: 122

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STREET: 1155 Avenue of the Americas

CITY: New York

STREET: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: 13-UN-1997

CLASSIFICATION NUMBER: US/08/874,825

FILING DATE: 13-UN-1997

CLASSIFICATION: A35

PRIOR APPLICATION DATA:
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             STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
OFERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-UN-1997
CLASSIPTCATION: 43.5
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/663,824
FILING DATE: 14-UN-1996
ATONNEY AGENT INFORMATION:
NAME: MISTOCK, S. LEGILE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-045
TELEPHONE: 212-790-9999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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STRANDEDNESS: single
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US-08-874-825-78
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New York
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Fatent No. 6083693

GENERAL INFORMATION

APPLICANT: Nordabalan, Krishnan

APPLICANT: Nordabalan, Krishnan

APPLICANT: Nordabalan, Krishnan

TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN

TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS

FILE REFERENCE: 7934-006

CURRENT APPLICATION NUMBER: US/08/663,824

CURRENT FILING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 78

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Patent No. 6083633

GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 794-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                 39.0%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 55; indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.0%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                7934-045
FILING DATE: 14-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18 872
REFERENCE/DOCKET NUMBER: 7934
TELECOMMUNICATION INFORMATION:
TELERAX: 212-796-9090
TELERAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs
TYPE: MUOLeic acid
STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 81.0.
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Sequence 79, Application US/09231303

Patent No. 6395476

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Nandabalan, Krishnan

APPLICANT: Nandabalan, Krishnan

TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN

TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

FILE REFERENCE: 794-087

CURRENT APPLICATION NUMBER: US/09/231,303

CURRENT FILING DATE: 1999-01-12

BARLIER PALICATION NUMBER: 08/663,824

BARLIER PALICATION OF PROFE : 1996-06-14

NUMBER OF SEQ ID NOS: 118

SSOFTWARE: Patentin Ver. 2.0

SEQ ID NO 79

LENGTH: 12
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UNIONAL 19.3

WESOUL

Sequence 79. Application US/09231303

Sequence 79. Application US/09231303

Patent No. 6395478

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Nandabalan, Krishnan

TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN

TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

TITLE APPLICATION NUMBER: US/09/231,303

CURRENT FILING DATE: 1996-01-12

EARLIER FILING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PATENTIN VANCE: 2.0

SEQ ID NO 78

SEQ ID NO 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: linker US-09-231-303-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7.8; DB 1; Length 12;
Pred. No. 55;
0; Mismatches 2; Indels
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                                                                   Score 7.8; DB 1; Length 12;
Pred. No. 55;
                                                                                                                      0; Mismatches
OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TGGACTCGCTG 12
                                                                                                                                                                  9 GCTGGCACGCA 19
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Best Local Similarity
       ; OLDER 1149-32
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Sequence 181. Application US/09281418

Patent No. 6287769

GENERAL INFORMATION:
TARRAZI INCORPATION:
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA FITLE OF INVENTION: method of Assaying Microorganisms, Method of Analyzing Mirrary Applicanton nisms and Method of Assaying Contaminant
TITLE OF INVENTION: member: US/09/281,418

TITLE OF INVENTION: misms and Method of Assaying Contaminant
FILE REFERENCE: 9982-7

CURRENT FILING DATE: 1990-03-30

EARLIER PEDLICATION NUMBER: UF/1999/69694

EARLIER PILING DATE: 1990-03-16

BARLIER PILING DATE: 1990-03-16

SEQ ID NOS: 216

SEQ ID NOS: 216

LENGTH: 12
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APPLICANT: Schmidt, Gunter
APPLICANT: Schmidt, Gunter
TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the
TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the
TITLE OF INVENTION: Identification of Antisense Binding Sites
TITLE OF INVENTION: UNBER: US/09/043,149
CURRENT APPLICATION NUMBER: US/09/043,149
FRIOR FILING DATE: 1996-09-13
PRIOR FILING DATE: 1996-09-13
PRIOR FILING DATE: 1996-09-14
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PREDICT NOS: 54
SOFTWARE: PREDICT NOS: 54
SOFTWARE: PREDICT NOS: 54
SOFTWARE: 12
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                                                                                            ; FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: linker US-08-663-824-79
                                                                                                                                                                                    Score 7.8; DB 1; Length 12;
Pred. No. 55;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 12;
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Pred. No. 55;
0; Mismatches
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US-09-043-149-32
'Sequence 32, Application US/09043149
'Patent No. 6355418
SEQ ID NO 79
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                         Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Primer
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US-09-281-418-181
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US-09-889-789-216

Sequence 2216, Application US/09989789

Patent No. 6589746

GENERAL INFORMATION:

APPLICANT: LIU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REPERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/9899,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0

LENGTH: 9
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA

ORGANISM: Artificial Sequence

PEATURE:

OTHER INFORMATION: Description of Artificial Sequence: example target

US-09-989-789-2216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: example target
COTHER INFORMATION: DNA
US-09-989-789-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pacent No. 6588746
GRNEAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRENCE: 8325-0011.20 / S11-US2
CURRENT APPLICANT: US/09/989,789
CURRENT FILING DATE: 2002-03-25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2286
LIBNGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.0%; Score 7.4; DB 1; Length 9; 88.9%; Pred. No. 3.6e+02; tive 0; Mismatches 1; Indels
  Indels
2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
9; Conservative
                                                                      1 recadrodord 11
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US-09-989-789-2287
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US-09-989-789-2286
Matches
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PREJECTAT: LITTLE OF INVENTION FOSITION DEPREDENT RECOGNITION OF GRN NUCLEOTIDE
TITLE OF INVENTION: FOSITION DEPREDENT RECOGNITION OF GRN NUCLEOTIDE
TITLE OF INVENTION: FOSITION OF STRIPERS BY ZINC FINGERS
FILE PREPERENCE: 8335-0011.00 (20.20)
FILE REPREDENCE: 8335-0011.00 (20.20)
FILE REPREDENCE:
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RESULT 95
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                                                               Score 7.4; DB 1; Length 10;
Pred. No. 55;
0; Mismatches 1; Indels
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                 ZIP: 80111
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOSTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,245
FILING DATE:
                                                                                                                                                                                                    Sequence 1, Application US/08309245
Patent No. 5723289
GENERAL INFORMATION:
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite
CITY: Englewood
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-170-290A-1
                                                               Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDURS: single ;
1 TOPOLOGY: linear
US-08-309-245-1
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                 11 TGGCACGCA 19
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                                                                                                                                          10 TGGCGCGCA 2
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US-08-309-245-1
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RESULT 94
US-08-462-389-1
Sequence 1, Application US/08462389
Patent No. 572592
GENERAL INFORMATION:

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APPLICANT: Galon, Bruce
APPLICANT: Galon, Bruce
APPLICANT: Gold, Galon
APPLICANTON
APPLICANT: Gold, Galon
APPLICANT: Gold, Galon
APPLICANT: Galon
APPLICANT: Gold, Galon
APPLICANT: Gold, Galon
APPLICANT: Gol
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: EDM compatible OPERATING SYSTEM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordParfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,700
FILING DATE: MACCA 20, 1996
PRIOR PREDICATION: NUMBER: 08/309,245
PILING DATE: 20-SEPTEMBER-1994
ATTORNEY/AGENT INFORMATION:
NAME: BATTON NUMBER: 33,215
RESERBNCE/DOCKET NUMBER: 33,215
RESERBNCE/DOCKET NUMBER: MEX22/PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                           MASULT 97
US-08-618-700-1
Sequence 1, Application US/08618700
Patent No. 585660
GENERAL INFORMATION:
TITLE OF INVENTION: PARALLEL SELEX
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Swanson & Bratschun, L.L.C.
SITRET: 8400 East Prentice Avenue, Suite #200
CITY: Brilewood
STATE: Colorado
COWITY: USA
ZIP: B0111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7.4; DB
Pred. No. 55;
0; Mismatches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.0%;
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Best Local Similarity 88.9
Matches 8, Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                             i LENGTH: 10

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-101-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              10 CTGGCACGC 18
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US-08-618-700-1
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US-08-461-418B-4
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: IBM compatible COMPUTER: Worderfect 6.0 (a) For Windows CURRENT ADALCATION DATA:

APPLICATION NUMBER: US/08/463,101

FILING DATE: 20.5EPTEMBER-1994

RAPLICATION DATA: 20.5EPTEMBER-1994

RAPLICATION DATA: 70/714,131

FILING DATE: 10.7UNE 1991

RAPLICATION NUMBER: 30/215

FILING DATE: 11.7UNE 1990

ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWAIDS: NEX22-1

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPROME: (303) 793-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-465-101-1
| Sequence 1, Application US/08463101
| Patent No. 5789160
| GENERAL INFORMATION:
| APPLICANT: Batcn, Bruce
| APPLICANT: Batcn, Larry
| TITLE OF INVENTION: PARALLEL SELEX
| NUMBER OF SEQUENCES: 3
| CORRESPONDENCE ADDRESSE: ADDRESSER: Swanson & Bratschun, L.L.C.
| STREET: 8400 East Prentice Avenue, Suite#200
| STREET: Colorado
| STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.0%; Score 7.4; DE 66.7%; Pred. No. 55; ative 2; Mismatches
FILING DATE: June 27, 1991
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01822
FILING DATE: 19 March 1991
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REBERENCE/DOCKET NUMBER: 151S-0309
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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2 CUCUCUGGC 10
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MOLECULE TYPE: Othe
HYPOTHETICAL: NO
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US-07-724-500B-4
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US-08-481-658B-21
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APPLICANT: Ecker et al.
TITLE OF INVENTION: Reagents And Methods For Modulating Gene
TITLE OF INVENTION: Expression Through RNA Mimicry
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5874564ris LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                     CIT:
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION DATA:
APPLICATION NUMBER: US/08/461,418B
FILING DATE: 05-10701-1992
FILING DATE: 16-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAMM: Paul K. Legaard
NAMM: Paul K. Legaard
STELERRALION NUMBER: 181S-199
TELECOMMUNICATION NUMBER: 181S-199
TELECOMMUNICATION NUMBER: 181S-199
TELEPHONE: 215-568-3439
TELEPHONE: 215-568-3439
TELEPHONE: 215-568-3439
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US-08-481-658B-21/C
| Sequence 21, Application US/08481658B
| Patent No. 5955075
| GENERAL INFORMATION:
| APPLICANT: Zavada, Jan
| APPLICANT: Zavada, Jan
| TITLE OF INVENTION: NN Gene and Protein
| TUTLE OF INVENTION: NN Gene and Protein
| NUMBER OF SEQUENCES: 86
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Leona L. Lauder
| STREET: 6 Mariposa Court
| CITY: Tiburon
| STREET: 6 Mariposa Court
| CITY: Tiburon
| STREET: 6 Mariposa Court
| COUNTRY: USA
| ZIP: 94920
| COMPUTER READABLE FORM:
| MEDIUM TYPE: Ploppy disk
| COMPUTER READABLE FORM:
| MEDIUM TYPE: Ploppy disk
| COMPUTER READABLE FORM:
| STREET: BN PC COMPATIBLE
| COMPUTER READABLE FORM:
| STREET: BN PC COMPATIBLE
| COMPUTER READABLE FORM:
| COMPUTER R
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37.0%; Score 7.4; DB
Best Local Similarity 66.7%; Pred, No. 55;
Matches 6; Conservative 2; Mismatches
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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US-08-461-418B-4
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FRIDE APPLICATION DRIN: gos/260,190

FILING DATE: ILLUM: 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lander, Lander
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Query Match

Best Local Similarity 88.9'
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                                     ; TITLE: "Human ;
; TITLE: consens;
; JOUNNAL: Natur;
; VOLUME: 1
; PAGES: 44-49
; DATE: 1992
US-08-486-756A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 102
US-08-485-862B-21/c
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MEDIUM TYPE: 1 Ploppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHING SYSTEM: 190 (8486,756A
FILING DATE: US 08/260,190
FILING DATE: US 08/260,190
FILING DATE: LS-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder: LS-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder: LS-JUN-1994
ATTORNEY/AGENT INFORMATION:
TELEPOMONICATION INFORMATION:
TELEFAX: 415-435-4034
TELECOMONICATION INFORMATION:
TELEFAX: 415-435-4034
TELECOMONICATION INFORMATION:
TELEPOMONICATION INFORMATION:
TELEPOMONICATION INFORMATION:
TELEPOMONICATION INFORMATION:
TELEPOMONICATION INFORMATION:
SEQUENCE CARACTERISTICS:
LENGTH: 10 base pairs
TYPE: mucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
BESCRIPTON INFORMATION:
TOPOLOGY: Linear
MOLECULE TYPE: DNA (Genomic)
BESCRIPTON INFORMATION:
PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.0%; Score 7.4; DB 1; Length 10;
88.9%; Pred. No. 55;
tive 0; Mismatches 1; Indels
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: mucleic acid
STRANDEDMESS: double
STRANDEDMESS: double
TOPOLOGY: linear
MOLECULE TYPE: DA (genomic)
DESCRIPTION: p53 binding site
PUBLICATION INFORMATION:
AUTHORS: R1 Delity et al.
TITLE: "Human genomic DNA sequences define a
TITLE: Consensus binding site for p53"
WOLTANDE: Nature Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MESULT 101
US-08-486-756A-21/C
Sequence 21, Application US/08486756A
FATEL No. 5931711
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.9
Matches 8; Conservative
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TITLE: Numeric generic BDM sequences define a TITLE: Numeric generic BDM sequences define a YOUTHAIL: Numeric generic BDM sequences define a YOUTHAIL: Numeric generic BDM SECONDERS. 1931

| YOUTHAIL: Numeric generic BDM SECONDERS. 1931
| YOUTHAIL: STATE BDM SECONDERS. 1932
| YOUTHAIL: STATE BDM SECONDERS. 1933
| YOUTHAIL: YOUTHA
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                                                                                                                                                                                                                                                                   RESULT 103
US-08-388-353-703
is Sequence 703, Application US/08388353
is Patent No. 6010895
is Patent No. 6010
Query Match 37.0%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 55; Matches 8; Conservative 0; Mismatches 1; Indels
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels
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Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Methee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deacon, Nicholas J.
Learmont, Jennifer C.
McPhee, Dalle A.
Crowe, Suzanne
Cooper, David
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US-08-388-353-703
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                                                                                                                                               3 GGACTCGCT 11
                                                                                                                                                                                                               10 GGACTAGCT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 104
US-08-388-353-704
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NUMERS OF SEQUENCES: 800 CARRESTORY OF HIV-1

NUMERS OF SEQUENCES: 800 CARRESTORY OF SEQUENCES: 800 CAR
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12 GGCACGCAC 20

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                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Learmont, Jennifer C.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Morbee, Dale A.
APPLICANT: Morbee, Dale A.
APPLICANT: Cooper, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDER ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STRET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7.4; DB
Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h Similarity 88.9%; Pred. No. 55; 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 106
US-08-388-353-770/c
; Sequence 770, Application US/08388353
; Patent No. 6010895
; GENERAL_INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 9606
TELECOMMULICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-436
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 769:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                      ; TYPE: nucleic acid
; TYPE: nucleic acid
; TRANUDENESS: single
; TOPOLOGY: linear
; MOLECTLE TYPE: DNA (genomic)
US-08-388-353-769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-388-353-770
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                  12 GGCACGCAC 20
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Best Local Similarity
Matches 8; Conserv
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Gaps
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                                                                                               US-08-408-518-703

US-08-408-518-703

Sequence 703, Application US/08488551B

Patent No. 60.15661

APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper

TITLE OF INVENTION:
NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY
STREET: A00 GARDEN CITY
STREET: U.S.A.
ZITE: NEW YORK
COUNTRY: U.S.A.
ZITE: SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ILSS-0.0299
COMPUTER: ID PC COMPALIA
MEDIUM TYPE: Floppy disk
COMPUTER: O'-JUN-1995
SPRING SYSTEM: O'-JUN-1995
PRIOR APPLICATION NUMBER: PM3064 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PN0384 (AU)
FILING DATE: 11-FEB-1994
APPLICATION NUMBER: PN0384 (AU)
FILING DATE: 11-FEB-1995
ATPOINTS JAPELICATION NUMBER: PN0384 (AU)
FILING DATE: 11-FAB-1995
ATPOINTS JAPELICATION NUMBER: PN0384 (AU)

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Pred. No. 55;
0; Mismatches 1; Indels
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US-08-488-551B-704
; Sequence 704, Application US/08488551B
; Patent No. 6015661
; GRNERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative (
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 CTCGCTGGC 14
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GGCACACAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-488-551B-703
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DB 1; Length 10;
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US-08-488-551B-770/C

IS SEQUENCE 770, Application US/08488551B

Fatent No. 6015661

GENERAL INFORMATION:

APPLICANT: Nicholas J. Deacon

APPLICANT: David Cooper

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SIQUENCES: 841

CORRESPONDENCE ADDRESS:

ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: AGO GRADEN CITY PLAZA

CITY: GARDEN CITY

STATE: NEW YORK

COUNTRY: US.A.

ZIP: 11530-0299

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENT: DEACALL NELEASE

STATE: 11530-0299

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: DEACALL NELEASE

FILLING DATE: 07-JUN-1995

PRIOR APPLICATION NUMBER: US/08/488,551B

FILLING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

PAPLICATION NUMBER: US/08/488,551B

FILLING DATE: 07-JUN-1995
      OPERATING STSTEM: PC-LOS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,51B
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM0204 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0204 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: PM0204 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 769:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7.4; DB
Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
FILING DATE: 21-FEB-1994
FILING DATE: 21-FEB-1994
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/389,353
APPLICATION NUMBER: US 08/389,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GGCACGCAC 20
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US-08-488-551B-769/C
Sequence 769, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. Wchee
APPLICANT: Worden C. STATE: SCOTT, WURPHY & PRESSER
CITY: GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: WW YORK
COUNTRY: D. S. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 10;
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                                                                                                                                                                                                                                                          COMPUTER: U. S. A.,

ZIP: 11230-0299

COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGFWARE: Patentin Release #1.0, Version #1.25
SUSPERMED: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/48,551B
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PN0201/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PN0201/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PN0201/95
TELECHOMUNICATION INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECHOMUNICATION INFORMATION:
TELEPAX: (516) 742-4343
TELEPAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 704:
FEMALICATION FOR SEQ ID NO: 704:
                          TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1 NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Pred. No. 55;
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
David Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CTCGCTGGC 14
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US-08-488-5518-704
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                                                                                                                                                                                                                     NEW YORK
: U.S.A.
                                                                                                                                                                                    CITY: GAR
STATE: NE
COUNTRY:
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Sequence 1, Application US/08793398

Patent No. 6030776

APPLICANT

APPLICANT

TILLE OF INVENTION: Parallel SELEX

TILLE OF INVENTION: Parallel SELEX

NUMBER OF SEQUENCES: 5

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/08/793,398
                                                                                                                                                                                                                                                                                                                                                                           37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 55; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/11982
FILING DATE:
APPLICATION NUMBER: US 08/309,245
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/714,131
FILING DATE: 10-JUN-1991
PRIOR APPLICATION DATA:
PRILING DATE: 11-JUN-1990
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.0%; Score 7.4; DE ilarity 88.9%; Pred. No. 55; Conservative 0; Mismatches
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-YAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGLGLO:
REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4346
INFORMATION FOR SEQ ID NO: 770:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE : nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Matches 8; Conservative
                                                                                                                                                                                                                                                                            single
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TYPE: nucleic acid
STRANDEDNESS: sing
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                   US-08-488-551B-770
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CAGGCACGC 10

RESULT 112

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: Diskette, 3.5 inch, 1.44 MB storage OPERATING SYSTEM: MS-108.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,601
FILING DATE: September 1,1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,700
FILING DATE: APPLICATION: DATA:
APPLICATION NUMBER: 08/309,245
FILING DATE: 20-SEPTEMBER-1994
ATTORNEY/AGENT NUMBER: 33,215
REPERENCE/DOCKET NUMBER: 33,215
REPERENCE/DOCKET NUMBER: MX22/CIP2
TELECOMMUNICATION INFORMATION:
NAME: BATY J. SWANBON: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
Sequence 1, Application US/09157601
Patent No. 6048698
GENERAL INFORMATION:
FAPFILICANT: EATON, BRUCE; GOLD, LARRY
TITLE OF INVENTION: PARALLEL SELEX
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: SWANSON & Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/08487077A

Patent No. 6069242

GENERAL INFORMATION:
PAPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorekova, Jaronir
ITLE OF INVENTION: WM Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCES: 86
CORRESPONDENCE ADDRESS:
CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Pred. No. 55;
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COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 CTGGCACGC 18
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CITY: Englewood
STATE: Colorado
COUNTRY: USA
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REGISTRATION NUMBER: 30,863
REGISTRATION NUMBER: D-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-0727
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANBENESS: double
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,863A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels
                                               Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
DESCRIPTION: p53 binding site
PUBLICATION INFORMATION:
AUTHORS: El Beiry et al.
TILLE: "Human genomic DNA sequences define a
TITLE: consensus binding site for p53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 114
US-08-485-863A-21/C
Sequence 21, Application US/08485863A
Sequence 3 Sequence 3, Application US/08485863A
Sequence 3, Application US/0848585B
STATE: California
COUNTRY: USA
                                          SOFTWARE: Patentin Release #1.0, Vers.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,077A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY ADANT INFORMATION:
NAME: LANGEY, LEGNA INFORMATION:
NAME: LANGEY, LEGNA INFORMATION:
TELEFRONCE/DOCKET NUMBER: D-0021.3H
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GGACTCGCT 11
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,049D
FILING DATE: 07-UW-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: La-UW-1994
ATTORNEY/AGENT IRFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: D-0021.33
REFERENCE/DOCKET NUMBER: D-0021.33
TELERBIONE: 415-2034
MEDIANDER: ALSORION:
TELERBIONE: 415-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 55; tive 0; Mismatches 1; Indels
                                                                                                                                                                                               TOOLOGY: under TOOLOGY: linear MOLECULE TYPE: DNA (genomic)
DESCRIPTION: DS3 binding site
PUBLICATION INFORMATION:
AUTHORS: E1 Deiry et al.
TITLE: consensus binding site for p53"
JOURNAL: Nature Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 115
US-08-485-049D-21/C
Sequence 21, Application US/08485049D
Patent No. 6204370
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 369 Pine Street
STREET: 369 Pine Street
STREET: California
COUNTRY: USA
D-0021.3G
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TYPE: nucleic acid
STRANDEDNESS: single
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US-09-989-789-567/c
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ADDRESSER: Wooddock Washburn Kurtz Mackiewicz & No. 6368863ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                   ö
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Patent No. 636863;
GENERAL INFORMATION:
TITLE OF INVENTION: Reagents And Methods For Modulating Gene;
Expression Through RNA Mimicry
                                                                                                                                                                                                                                                                                                   .;
0
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Pred. No. 55;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                               DB 1; Length 10;
                                                                                                                                                                                                                                                                                                   1; Indels
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Sequence 2-0. Application US/08899241A
Sequence 2-0. Application US/08899241A
SEREAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Huembelin, Markus
APPLICANT: CALLICAN LOON, Adolphus
APPLICANT: Schurter, Walter
ITILE OF INVENTION: Improved Riboflavin Prod
CURRENT APPLICATION NUMBER: US/08/899,241A
CURRENT FILING DATE: 1997-07-23
EARLIER APPLICATION NUMBER: 95111905.4
EARLIER PILING DATE: 1996-07-24
NUMBER OF SEQ ID NOS: 252
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 2-201
               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: p53 binding site
PUBLICATION INFORMATION:
AUTHORS: El Deiry et al.
TITLE: "Human genomic DNA sequences define
TITLE: consensus binding site for p53"
VOLUME: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
                                                                                                                                                                                                                                                             Score 7.4; DB
Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.0%;
88.9%;
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: PA
COUNTRY: U.S.A.
double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ACTCGCTGG 13
                                                                                                                                                                                                                                                                                                                                       3 GGACTCGCT 11
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US-08-899-241-240
                                                                                                                                                                                PAGES: 44-49
; DATE: 1992
US-08-485-049D-21
 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 116
US-08-899-241-240/c
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US-09-255-899-4
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Gaps
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OTHER INFORMATION: Description of Artificial Sequence: example target
OTHER INFORMATION: DNA
US-09-989-789-567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 567, Application US/09989789

Patent No. 5588746

GENERAL INFORMATION:
APPLICANT: LIU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: PRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 568, Application US/09989789
Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,899
FILING DATE: 23-Feb-1999
CLASSIFICATION NUMBER: US/09/255,899
FILING DATE: 23-Feb-1999
CLASSIFICATION NUMBER: 08/461,418
FILING DATE: *UNKnown>
APPLICATION NUMBER: 08/461,418
FILING DATE: *UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: PAUL K. LEGGARG
RECISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1998
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLCGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 497,090
FILING DATE: MAICH 21, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REPERENCE/DOCKET NUMBER: 32,257
REPERENCE/DOCKET NUMBER: 1S15-
TELECOMMUNICATION INFORMATION:
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 66.7
Matches 6; Conservative
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEIC ACID
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      2 CUCUCUGGC 10
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COUNTRY: U
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                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
CTHER INFORMATION: DNA
US-08-989-789-568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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APPLICANT: Ecker et al.

APPLICANT: Ecker et al.

TITLE OF INVENTION: REAGENTS AND METHODS FOR MODULATING
TITLE OF INVENTION: GENE EXPRESSION THROUGH RNA MIMICRY
NUMBERS OF SEQUENCES:

ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Wacklewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STREET: DESKETTE: PC-DOS
COUNTRY: USA
ZIP: 19103
COMPUTER: IBM PS/2 DISKETTE; 3.5 INCH, 1.44 Mb STORAGE
CONTURY: IBM PS/2 DISKETTE: SOOFWARE: WORDEREFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01822A
FILING DATE: March 21, 1990
ATTOREY/DOCKET NUMBER: ISIS-0109
TELEFRANCE CHARACTERISTICS:
TELEFRANCE CHARACTERISTICS:
TELEFRANCE CHARACTERISTICS:
TWO TELEFRANCE CHARACTERISTICS:
THE MATCH TO THE MATCH TO
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Pred. No. 55;
0; Mismatches 1; Indels
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TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS FILE REFERENCE: 8325-0011.20 / S11-US2 CURRENT APPLICATION UNDER: US/09/989,789 CURRENT FILING DATE: 2002-03-25 NUMBER OF SEQ ID NOS: 4085 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 LENGTH: 10
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37.0%; Score 7.4; DB
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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STRANDEDNESS: single
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66.7%; Pred. No. 55;
tive 2; Mismatches 1; Indels
Sequence 4, Application PC/TUS9102628
GENERAL INFORMATION:
APPLICANT: Ecker et al.
TITLE OF INVENTION: REAGENTS AND METHODS FOR MODULATING
TITLE OF INVENTION: GENE EXPRESSION THROUGH RNA MIMICRY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                              ZIP: 19103
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IEM PS/2
COMPUTER: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: DISKETTE, 5.0
SOFTWARE: PC-DOS
SOFTWARE: WORDPREFECT 5.0
CURRENT APPLICATION DATA:
FILLING DATE: 19910417
CLASSIFICATION: 536
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: 1BM compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9511982
GENERAL INFORMATION:
APPLICANT: EATON, BRUCE; GOLD, LARRY
ITILE OF INVENTION: PARALLEL SELEX
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Swanson & Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
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37.0%;
88.9%;
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88.9%;
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Best Local Similarity 88.5
Section 8, Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
                                       10 CTGGCACGC 18
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TITLE OF INVENTION: Parallel SELEX
NUMBER OF SEQUENCE: 5
COMPUTER: BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: ICATION NUMBER: US 07/714,131
FILING DATE: 10-UNN-1991
PRIOR APPLICATION NUMBER: US 07/536,428
FILING DATE: 11-UNN-1990
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS: 1:
LENGTH: 10 base pairs
TYPE: nucleic acid
companiements
COMPUTER: Compatible
COMPUTER: COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.4; DB 1; Length 10;
Pred. No. 55;
0; Mismatches 1; Indels
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                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEX22/PCT
                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/309,245
FILING DATE: 20-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/14,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/556,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: BARRY J. SWARNSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: 0222/PC
TEMECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9511982A GENERAL INFORMATION:
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88.9%;
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WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 CIGGCACGC 18
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Sequence 89, Application US/09249155A

Patent No. 6538173

GENERAL INFORMATION:

APPLICANT: Heber-Katz, Ellen

TITLE OF INVENTION: Compositions and Methods for Wound

TITLE OF INVENTION: Healing

FILE REFERENCE: 00486.7862A

CURRENT APPLICATION NUMBER: US 60/074,737

PRIOR APPLICATION NUMBER: US 60/074,737

PRIOR APPLICATION NUMBER: US 60/097,937

PRIOR APPLICATION NUMBER: US 60/097,937

PRIOR APPLICATION NUMBER: US 60/102,051

PRIOR PRIOR DATE: 1998-09-28

NUMBER OF SEQ ID NOS: 346

SOFTWARE: PASESQ for Windows Version 4.0

LENGTH: 11
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Sequence 177, Application US/09249155A

Patent No. 6538173

GENERAL INCRMATION: Compositions and Methods for Wound
TITLE OF INVENTION: Compositions and Methods for Wound;
TITLE OF INVENTION: Compositions and Methods for Wound;
TITLE OF INVENTION: Healing
FILE REFERENCE: 00486.78503

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,737

PRIOR PILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-26

PRIOR FILING DATE: 1998-08-26

PRIOR FILING DATE: 1998-08-26

NUMBER OF SEQ ID NOS: 346

SOFTWARE: FRAEESEQ for Windows Version 4.0

LENGTH: 11
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Gaps
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| Sequence 19. Application US/08484408A
| Patent No. 6117653
| GENERAL INFORMATION:
| APPLICANT: Thoma, Hans A
| TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
| NUMBER OF SEQUENCES: 56
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Popovich & Wiles, P.A.
| STREET: 80 S. 8th Street, Suite 1902
| CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.0%; Score 7; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 0; Indel®
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMILM Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: POPPOVICE, Thomas E
REGISTRATION NUMBER: 30,099
                                            CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC compatible
COMPUTE: IBM PC compatible
COMPUTE: BEADABLE FORM:
COMPUTE: IBM PC compatible
COMPUTE: BEADABLE FORMS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PRUL, THOMAS D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPRONE: 713/651-5246
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPOPLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGACT 7
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LOCATION: 5..8
OTHER INFORMATION: from cligonucleotide duplex formation with nucleotides 4-7 of
OTHER INFORMATION: Erom cligonucleotide duplex formation with nucleotides 4-7 of
OTHER INFORMATION: SEQ ID NO: 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Patent No. 60835655

APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul B.
ITILE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
                                               0S-08-480-173A-18/c
| Sequence 18, Application US/08480173A
| Patent No. 6072049
| Cabusal Information:
| APPLICANT: Thoma, Hans A
| TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE NUMBER OF SEGUENCES: 56
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                             CUNTRY: MINEAPOLIS

COUNTRY: USA

COUNTRY: USA

COMPUTE: SEADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,173A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 4095

ATTORNEY/AGENT INTORNATION:

NAME: POPOVICh, Thomas E

REFIRENCE/DOCKET NUMBER: 30,099

REFERENCE/DOCKET NUMBER: 30,099

REFERENCE/DOCKET NUMBER: 991

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPPINGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..4
COCHER INFORMATION: /note= "Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end""
                                                                                                                                                                                                                                                          ADDRESSEE: Popovich & Wiles, P.A. STREET: 80 S. 8th Street, Suite 1902 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 7; Conservative
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US-08-859-954-148
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Gaps
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; OTHER INFORMATION: Description of Artificial Sequence:Primer US-09-398-499-24
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                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence:Primer US-09-398-499-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indeli
                                                                                                                                                                                                                                                                                     Query Match

35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indeli
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US-09-398-499-29/C
US-09-398-499-29/C
Sequence 29, Application US/09398499
Patent No. 6284466
GENERAL INFORMATION:
APPLICANT: Benson, Andrew K.
TILLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
TILLE OF INVENTION: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1999-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Senson, Andrew K.

TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REFERENCE: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1999-09-18
SOFTWARE: PATENTIN VOICE: 58
SOFTWARE: PATENTIN VOICE: 2.1
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-398-499-24/c
; Sequence 24, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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LENGTH: 8
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LENGTH: 8
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THER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 4-7 of
OTHER INFORMATION: SEQ ID NO: 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.0%; Score 7; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09398499;
Patent No. 6284466;
GENERAL INFORMATION:
APPLICANT: BENERO, Andrew K.
TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REPRENCE: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499;
CURRENT FILING DATE: 1999-09-17
FRIOR FILING DATE: 1999-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 8
                                                                                                                                                                                                                                                                     RESULT 130
US-09-388-499-6
US-09-388-499-6
Sequence 6, Application US/09398499
Sequence No. 6284466
GENERAL INFORMATION:
APPLICANT: Benson, Andrew K.
TITLE OF INVERTION: HIGH RESOLUTION GENOME SCANNING
FILE REFERENCE: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
35.0%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 4.1
Matches 7; Conservative 0; Mismatches
    MED1003USD4
REFERENCE/DOCKET NUMBER: MEDI
TELECOMUNICACION INFORMATION:
TELEPHONE: 612-334-8991
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
                                                                                                                                                                                       PARALUSE:
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 5..8
                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 CGCTGGC 14
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US-09-398-499-1
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TYPE: DNA ORGANISM: Artificial Sequence
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US-09-154-750A-41
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                                                                                                                          RESULT 133
US-08-362-495-3/C
; Sequence 3, Application US/08362495
; Sequence 3, Application US/08362495
; Patent No. 60871711
; GENERAL INFORMATION:
APPLICANT: Neuman, Toomas
; APPLICANT: No. 60871711nes, Howard O.
; TITLE OF INVENTION: METHOD FOR INDUCING DNA SYNTHESIS IN
TITLE OF INVENTION: METHOD FOR INDUCING DNA SYNTHESIS IN
TITLE OF INVENTION: METHOD FOR INDUCING DNA SYNTHESIS IN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
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                                                                                    0; Indels
                                          Query Match 35.0%; Score 7; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 0; Indel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY.

COUNTRY.

ZIP: 2005-3315

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM:

PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,495

FILNG DATE: 19-NOV-1996

CLASSIFICATION NUMBER: WP PCT/US94/14614

PRIOR APPLICATION NUMBER: WS PS/14614

PRIOR APPLICATION NUMBER: US 08/301,416

FILING DATE: 09-DEC-1994

PRIOR APPLICATION NUMBER: US 08/301,416

FILING DATE: 08-SEP-1994

PRIOR APPLICATION NUMBER: US 08/169,522

FILING DATE: 15-DEC-1993

ATTONINEY/AGENT INFORMATION:

ANAME: LABOR DATE: 15-DEC-1993

ATTONINEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,013
PPR: 05800.0001-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REPERENCE/DOCKET NUMBER: 056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 TGGCACG 17
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US-09-398-499-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-362-495-3
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CRGANISM: Artificial Sequence
PEATURE:
COTHER INFORMATION: Description of Artificial Sequence: example target
COTHER INFORMATION: DNA
US-09-989-789-2378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sequence 2378, Application US/09989789
Factor No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiana
TITLE OF INVENTION:
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.9: 4085
SEQ ID NO.9: 4085
SEQ ID NO.9: 0378
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; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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US-09-398-499-53/C

Sequence 53, Application US/09398499

Patent No. 6284469

Patent No. 6284460

TITLE OF INVEXTION: HIGH RESOLUTION GENOME SCANNING

TITLE REFERENCE: UNL 2963

CURRENT FILING DATE: 1999-09-17

PRIOR FILING DATE: 1999-09-17

PRIOR FILING DATE: 1998-09-18

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIN Ver. 2.1

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.0%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 66; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4.1. Application US/09154750A
; Batent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: VOGelstein, Bert
; APPLICANT: Finzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: P53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
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TELEX: 236925
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
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Best Local Similarity 80.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGACTCGC 10
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HANTI-SENSE: NO
US-08-750-655-1
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US-09-769-482-33/C
US-09-769-482-33/C
Sequence 33, Application US/09769482
Patent No. 656130
GARBEAL INFORMATION:
APPLICANT: NOUL, JUDD W.
TITLE OF INVENTION: PROSTATE SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: PROSTATE SPECIFIC ANDROGEN-SIGNALING ASSOCIATED
TITLE OF INVENTION: 040000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT APPLICATION NUMBER: 60/178,772
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR PILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
LENGTH: 10
                                                                                                                                                                                                                                                                                                                               Gaps
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US-09-475-947A-182/C
; Sequence 182, Application US/09475947A
; Patent No. 647154
; GENERAL INFORMATION;
; APPLICANT: Garner, Harold R.
; APPLICANT: Minna, John D.
; APPLICANT: Winna, John D.
; TILLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: US9067
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; SOFTWARE: Patentin Ver. 2.1
; SEGID ON 182
                                                                                                                                                                                                                                                                                   Query Match 35.0%; Score 7; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 66; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
35.0%; Score 7; DB 1.
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches
CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/059,153
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 91
LENGTH: 10
                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        4 GACTCGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 CACGCAC 20
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CRGANISM: human
US-09-475-947A-182
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CREANISH: Artificial Sequence

CREANISH: Artificial Sequence

OTHER HYDORATION: Description of Artificial Sequence: Synthetic

OTHER HYDORATION: Description of Artificial Sequence: Synthetic

OGNET ARTIFICATION TO STATE AND SECRET AND SECRET
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Patentin Release #1.0, Version #1.25 ICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDRES: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.0
Best Local Similarity 80.0
Matches 8; Conservative
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                          APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Croper, David
TITLE OP INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 670, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzame
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: ULLILOW COUNTRY: ULLILOW COUNTRY: LISSO
COMPUTER: READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLESSIFICATION: 424
ATTORNEY/AGENTINO: Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 3606
TELESCOMMULCATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFRAX: (516) 742-4343
TELEFRAX: (516) 742-4366
TELEFRAX: (510) 742-4313
TELEFRAX: (510) 742-4366
TELEFRAX: (510) 742-4313
TELEFRAX: (510) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Scully, Scott, Murphy & Presser: 400 Garden City Plaza
Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.0%; Score 6.8; DB
80.0%; Pred. No. 73;
tive 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States
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Best Local Similarity
Matches 8; Conserva
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US-08-388-353-670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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34.0%; Score 6.8; DB 1; Length 10; B0.0%; Pred. No. 73;
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Sequence 771, Application US/0838353

Petent No. 6010895

Petent No. 6010895

APPLICANT: Deacon, Nicholas J.

APPLICANT: Learmont, Jennifer C.

APPLICANT: Crowe, Suzane

APPLICANT: Crowe, Suzane

APPLICANT: Crowe, Suzane

APPLICANT: Crowe, Suzane

APPLICANT: Coper, David

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 800

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORFTAKE: BAEGAIL Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Diciplio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPAN: (516) 742-4343
TELEFAN: (516) 742-4366
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4366
TELECOMMUNICATION POR SEQ ID NO: 771:
SEQUENCE CHARACTERISTICS:
TEMMETHY 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: United
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US-08-488-551B-670
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                                                                                                            Gaps
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                                                                DB 1; Length 10;
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                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                          Sequence 669, Application US/08488551B
Fatent No. 601561
Fatent No. 601561
GENERAL INFORMATION:
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TILLS OF INVENTION: NOV-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STREET: NEW YORK
COUNTRY: U S.A.
ZIP: 11530-0299
COMPUTER: READBALE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: BIN PC Compatible
CORRESTING SYSTEM: PC-DOSS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 07-008-109

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: PM4002 (AU)

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: PM4002 (AU)

FILING DATE: 21-FEB-1994

APPLICATION NUMBER: PM4002 (AU)

FILING DATE: 21-FEB-1994

APPLICATION NUMBER: PM3021/95

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

ATTORNEY/AGBNT INFORMATION:

NAME: FRANK S. DIGTGLIO

REFERENCE/DOCKET NUMBER: 96062

TELEPHONE: (516) 742-4343

TELEPHONE: (516) 742-4343

TELEPHONE: (516) 742-4316

SEQUENCE CHARATERISTICS:

LEMATH. 10 has a paire
                                                              Score 6.8; DB
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 6.8; DE
Pred. No. 73;
0; Mismatches
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                           Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGACTCGCTG 12
                                                                                                                                                10 CTGGCACGCA 19
                                                                                                                                                                                            10 CGGGCACACA 1
                                                                                                                                                                                                                                                          RESULT 143
US-08-488-551B-669
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Sequence 670, GOLISED
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATI NATIONAL JUNCTURES, A DESCON
APPLICATI NATIONAL DATA OF THE SERVER
TRAINING TO COMPANY.
TRAINING THE SERVER OF THE SERVER
TRAINING STREET AND CARRENT OF THE SERVER
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RESULT 144

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Gaps

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US-08-878-835A-6/c

Sequence 6, Application US/08878835A

Sequence 6, Application US/08878835A

Patent No. 6337071

GENERAL INFORMATION:
APPLICANT: William Mitchell Molyneux
TITLE OF INVENTION: Mosquito and/or Flea Control
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: D. Peter Hochberg CO., L.P.A.
STREET: The Baker Building - Sixth Floor 1940 East 6th Street
STATE: Ohio
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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US-08-297-395-59

i Sequence 59, Application US/08297395A

i Patent NO. 6039947

i GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
APPLICANT: Howard A. Hafler
ITILE OF INVENTION: EPTIDES DERIVED FROW IMMUNODOWINANT
ITILE OF INVENTION: PEPTIDES OF MYSLIN BASIC PROTSIN
ITILE OF INVENTION: 1994-08-11
EARLIER APPLICATION NUMBER: US/08/297,395A

CURRENT FILING DATE: 1993-05-06

EARLIER FILING DATE: 1993-05-06

EARLIER PRILING DATE: 1993-03-0

EARLIER PRILING DATE: 1993-03-30

EARLIER PILING DATE: 1993-05-05

EARLIER PILING DATE: 1993-06-24

EARLIER PILING DATE: 1993-06-24

EARLIER PILING DATE: 1989-06-24

EARLIER PILING DATE: 1980-06-24

EARLIER PILING DATE: 1980-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%; Score 6.8; DB 80.0%; Pred. No. 73; tive 0; Mismatches
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMUNICATION INFORMATION:
TELEFRONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 864:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base palrs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                      US-08-757-024-864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-297-395-59
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Patent No. 6025339

GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Charlotte
STATE: No. 6025339th Carolina
CONTRY: USA
ZIP: 28234
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
TLANSIFICATION: 514
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOBTWARE: Batentin Release #1.0, Version #1.25
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 10-78B-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-78B-1994
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 21-78B-1995
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 14-78B-1995
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 17-78B-1995
ATTORNEY/AGENT INFORMATION:
TELEPHANE: (516) 742-4364
INFORMATION FOR SEQ ID NO: 771:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TELENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6.8; DB
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0
Matches 8; Conservative
         STATE: NEW YORK COUNTRY: U.S.A. ZIP: 11530-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 CTGGCACGCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 146
US-08-757-024-864
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Gaps

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APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
TITULE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
TITULE OF INVENTION: Method for Synthesizing CONA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
PRIOR APPLICATION NUMBER: US/09/508,753B
PRIOR PILING DATE: 1997-09-18
NUMBER: OF SEQ ID NOS: 472
LENGTH: 10
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Atra SHIMMOTO
APPLICANT: Atra SHIMMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Yuko SHIBATA
APPLICANT: Biji OHARA
APPLICANT: Biji OHARA
APPLICANT: Masanori WATAHIKI
APPLICANT: MOSANORI WATAHIKI
APPLICANT: MOSANORI WATAHIKI
APPLICANT: MOSANORI WATAHIKI
APPLICANTION NUMBER: US/09/508,753B
CURRENT APPLICATION NUMBER: US/09/508,753B
FILE REFERENCE: 01062/46
PRIOR PLING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
MUMBER OF SEQ ID NOS: 472
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.0%; Score 6.8; DB 1; Length 10; 80.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-508-753B-387/c
; Sequence 387, Application US/09508753B
; Patent No. 6544736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-508-753B-389

. Sequence 389, Application US/09508753B

. Patent No. 6544736

. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Akira SHIMAMOTO
APPLICANT: Yako SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Biji OHARA
APPLICANT: MASANORI WATAHIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Sequence 195, Application US/09508753B

Sequence 195, Application US/09508753B

Sequence 195, Application US/09508753B

Sequence 195, Application Sequence

APPLICANT: With SHIMAMOTO

APPLICANT: With SHIMAMOTO

APPLICANT: Hiroko FUNAKI

APPLICANT: Hiroko FUNAKI

APPLICANT: Masanori WarhHKI

APPLICANT: Masanori WarhHKI

TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

FILE REFERENCE: 00162/HG

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT PILING DATE: 1997-09-18

FRICK FILING DATE: 1997-09-18

NUMBER OF SEQ ID NOS: 472

LENGTH: 10
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                                                                                                                                                                        ZIP: 44114

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MByte storage COMPUTER: Diskette, 3.5 inch, 1.44 MByte storage COMPUTER: Diskette, 3.5 inch, 1.44 MByte storage COMPUTER: DBM Compatible w/ Pentium Processor OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: Microsoft Word 97

CURRENT APPLICATION DATA: More 1997

FILING DATE: June 19, 1997

CLASSIFICATION: 800

PRIOR APPLICATION: 800

CLASSIFICATION DATA: AV PO 6605

FILING DATE: 21 June 1996

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LEWATH: 10

TYPE: Nucleic Acid

TYPE: Nucleic Acid

TYPE: Nucleic Acid
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Pred. No. 73;
0; Mismatches 2; Indels
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80.0%; Pred. No. 73;
tive 0; Mismatches 2
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Sequence 289, Application US/09508753B

Patent No. 6544736

GENERAL INFORMATION:
APPLICANT: Attra SHINAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yasuhiro SHIBATA
APPLICANT: YUKO SHIBATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: UP 9/270324
PRIOR FILING DATE: 1997-09-18
SEQ ID NOS: 472
LENGRH: 10
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                                                                                                                                                                                                                                                                                   FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-389
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 153
US-08-894-454-132
is-08-894-454-132
sequence 132, Application US/08894454
general INFORMATION:
APPLICANT: VAN DEN VEN, W.J.M.
APPLICANT: SCHOENMAKERS, H.F.P.M.
ITILE OF INVENTION: MULTIPLE-TUMOR ABERRENT GROWTH
ITILE OF INVENTION: GENES
NUMBER OF SEQUENCES: 164
CORRESPONDERS ADDRESS:
ADDRESSEE: The Webb Law Firm
STREET: 700 Koppers Building, 436 Seventh Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TIPE: DIBRECTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTERED for Windows Version 2.0
SOFTWARE: FESTERED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,454
FILING DATE: 15-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/EP/00716
FILING DATE: 17-FEB-1996
APPLICATION NUMBER: 95200390.3
FILING DATE: 17-FEB-1995
APPLICATION NUMBER: 95201951.1
FILING DATE: 14-ULL-1995
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Johnson, Barbara E
REGISTRATION NUMBER: 31,198
REFERENCE/DOCKET NUMBER: 702-971100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 412-471-8815
TELEFAX: 412-471-4094
                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 15219-1818
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GGACTCGCTG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAATCGCTG 10
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CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: STIVASTAVA, SHIV
APPLICANT: MOUL, UDDD W.
APPLICANT: MOUL, UDDD W.
APPLICANT: WUL, UDDD W.
APPLICANT: WUL, UDDD W.
APPLICANT: SEGAWA, TAKEHIKO
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
TITLE OF INVENTION: WHERE: US/09/769, 482
CURRENT FAPLICATION NUMBER: 60/178, 772
PRIOR APPLICATION NUMBER: 60/178, 772
PRIOR APPLICATION NUMBER: 60/179, 045
PRIOR PILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATCHILING OF SECOND OF SECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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US-09-989-789-1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                          Gaps
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Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIV, Giang
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
TITLE OF INVENTION: 1001-03-03-03-05
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1268
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 10;
Score 6.8; DB 1; Length 10;
Pred. No. 73;
                                                                                     Indels
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34.0%; Score 6.8; DE
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches
                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-769-482-49/c
; Sequence 49, Application US/09769482
; Patent No. 6566130
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ORGANISM: Artificial Sequence
34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity Bu.v.
Best Local Similarity
'...
8; Conservative
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US-09-989-789-1268
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1 ATGGACTCGC 10

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32.0%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 4.18+02; tive 0; Mismatches 1; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FLING DATE:
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 32,714
REPERBNCE/DOCKET NUMBER: 32,714
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Paul, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.0 Query Match
Best Local Similarity 97.5 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGACTC 8
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US-08-859-954-202/c
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US-08-859-954-178
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| Sequence 178, Application US/08859954 |
| Sequence 178, Application US/08859954 |
| Patent No. 6083695 |
| Patent No. 6083695 |
| APPLICANT: Hardin, Susan H. |
| APPLICANT: Hardin, Paul E. |
| APPLICANT: Hardin, Paul E. |
| TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 56 |
| NUMBER OF SEQUENCES: 56 |
| SORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Full-sight & Jaworski L.L.P. |
| STREET: 1301 McKinney, Suite 5100 |
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                                                                                                                                                                                                                                                                                                        APPLICANT: SELBIE, Lisa
APPLICANT: SELBIE, Lisa
APPLICANT: HERZOG, Herbert
APPLICANT: SHINE, John
TITLE OF INVENTION: Human Neuropeptide Y-Y1 Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: 555 13th St, N.W., Suite 701-East
STREET: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20004
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.24
COMPUTER: Patentin Release #1.24
CURRENT APPLICATION DATA:
RPELICATION NUMBER: US/08/232,144
FLING DATE: Ze-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ERRNST, Barbara G
REGISTRATION NUMBER: 1871-107A
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TODOLOGY: Linear
TODOLOGY: Linear
TODOLOGY: Linear
                                                                                                                                                                                                                Sequence 10, Application US/08232144
Patent No. 5571695
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston
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    US-08-859-954-210
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US-08-859-954-212
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Sequence 210, Application US/08859954
Fetent No. 608369;
Patent No. 608369;
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof, NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: US.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
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DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEX/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEBHONE: 713/651-5325
TELEBHONE: 713/651-5326
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACT
                                  REFERENCE/DOCKET NUMBER: D-5900
TELECOMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEPAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERLESTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REGISTRATION NUMBER: 32,714
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US-08-859-954-202
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Patent No. 6083695
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Handin, Susan H.
APPLICANT: Hardin, Paul B.
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
Query Match
32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.0%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 4.1e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1301 MCKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMONIVACATION INFORMATION:
FELEPHONE: 713/651-5325
""TELEPHONE: 713/651-5325
""TELEPHONE: 713/651-5325
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US-08-859-954-213/c
; Sequence 213, Application US/08859954
; Patent No. 6083695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 8 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.0
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                           4 GACTCGCT 11
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GENERAL INFORMATION:

APPLICANT: Hardin, Susan H.

APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Raul E.

TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
NUMBER OF SEQUENCES: 566
NUMBER OF SEQUENCES: 666
NUMBER NUMBER: PCODS/MS-DOS
NOFTWARE: PATENTIN Release #1.0, Version #1.30
NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Patent No. 6083695
GRNERAL INPORMATION:
GRNERAL INPORMATION:
APPLICANT: Hardin, Suean H.
APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Paul B.
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pulbright & Jaworski L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.0%; Score 6.4; DB 1; Length 8; Best Local Similarity 87.5%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Fulbright & Jaworski L.L.P. 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D. 714
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEPAX: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1301 McKinney.
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGACTC 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-859-954-213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-859-954-403
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US-09-398-499-8
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09398499;
Patent No 6284466;
GENERAL INFORMATION:
APPLICANT: Benson, HIGH RESOLUTION GENOME SCANNING
TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REFRENCE: UNL 298: US/09/398,499;
CURRENT APPLICATION NUMBER: 60/101,011
PRIOR PILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 8
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                      32.0%; Score 6.4; DB 1;
87.5%; Pred. No. 4.1e+02;
live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.0%; Score 6.4; DB 1;
87.5%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-403
                                                                               RESULT 164
US-09-398-499-16
; Sequence 16, Application US/09398499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 8/...
7, Conservative
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TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-39
                                                                                                                                     Query Match
32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6.4; DB 1; Length 9; Pred. No. 3.6e+02; 0; Mismatches 1; Indels
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US-08-717-526-61
US-08-717-526
Sequence 61, Application US/08717526
Patent No. 5786147
GENERAL INFORMATION:
APPLICANT: RABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                 10 CTGGCACG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                             8 crescece 1
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US-08-488-015B-9
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   SEQ ID NO 39
LENGTH: 8
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, OTHER INFORMATION: Description of Artificial Sequence:Primer US-09-398-499-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:Primer US-09-398-499-31
                                                                                                                                                                                                                                                                                                                                        32.0%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 4.1e+02; ttive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.0%; Score 6.4; DB 1; Length 8; Best Local Similarity 87.5%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/09398499;
Patent No. 6284466;
GENERAL INFORMATION:
APPLICANT: Benson, Andrew K.
TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REPRENCE: UNL 2983;
CURRENT APPLICATION NUMBER: 1999-09-17;
FRIOR PEDICATION NUMBER: 60/101,011
PRIOR PILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
Patent No. 6284466

GREERAL INFORMATION:
APPLICANT: Benson, Andrew K.
TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REPRENCE: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499
CURRENT PILING DATE: 1999-09-17
FRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTING OF SEQ ID NOS: 58
SOFTWARE: PATENTING OF SEQ ID NOS: 58
SEQ ID NO 16
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application US/09398499
Fatent No. 6284466
GENERAL INFORMATION
ADAPLICANT: Benson, Andrew K.
TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REFERENCE: UNL 2963
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1999-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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US-09-398-499-39/c
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US-09-398-499-31/c
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REGISTRATION NUMBER: 30,024
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RDNESS: Bingle
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VESULI 1019

VESULI 1019

VESULI 1019

VERNERAL INFORMATION:

APPLICANT: Mallet, Francois

APPLICANT: Guillou-Bonnici, Francoise

APPLICANT: Cleutain, Philippe

APPLICANT: Levasseur, Pierre

TITLE OF INVENTION: MODIFIED PROMOTER FOR RNA POLYMERASE.

TITLE OF INVENTION: HAS PERATION AND ITS APPLICATIONS

NUMBER OF SEQUENCES: 65

CORRESSOURCES: 65

CONTRY: Alexandria

STATE: VA

COUNTRY: USA

ZIPP: 2214

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopyy disk

COMPUTER: DAP PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFFWARE: Parent In Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/360,051A

FILING DATE: 20-DEC-1994

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TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSED: OLIFF & BERRIDGE
STREET: 700 SOUTH WASHINGTON STREET
CITY: ALEXANDRIA
STATE: VA
CUNTRY: USA
ZATE: VA
COUNTRY: USA
COUNTRY: USA
COMPUTER: FIDAPY disk
COMPUTER: PIDAPY disk
COMPUTER: PIDAPY disk
COMPUTER: PIDAPY disk
COMPUTER: PADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DATE PROPOSINE: DOS/MS-DOS
SOFTWARE: PATENTIN FOLOS/MS-DOS
SOFTWARE: PATENTION: USAPI.
APPLICATION NUMBER: USAPI.
APPLICATION NUMBER: WEB 38732
TELERBHONE: ADS-SOFTWARTION:
TELERBHONE: 703-836-6400
TELERBHONE: ON-SEC ID NO: 61:
SROCHARTION FOR SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-717-526-61
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BETTIGGE, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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| TEREBRINGINGINGER NUMBER | Web 36049 |
| TEREBROWENTIATION INFORMATION | TOTAL | TOT
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US-08-934-097A-48/C
; Sequence 48, Application US/08934097A
; Patent No. 6210880
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Structure Probing With Structure-Bridging
; TITLE OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
                                                                                                                                         Sequence 48, Application US/09034205

Sequence 48, Application US/09034205

Patent No. 6194149

GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Fors, Lance P.
ITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/09/034,205
FILING DATE:
CLASSIFICATION: Kamrin T.
REGISTRATION NUMBER: 38,230
REFRENCY/DOCKET 188.38,230
REFRENCY/DOCKET NUMBER: PORS-03268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: mucleic acid
STANDEDUBS: single
STANDEDUBS: linear
MOLECULE TYPE: other nucleic acid
JENGTH: JENGTH: JENGTH NUMBER: COLOGY: Linear
MOLECULE TYPE: other nucleic acid
JESCALPTION: /desc = "DNA"
US-09-034-205-48
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Best Local Similarity 87.5
Matches 7; Conservative
TGGCACGC 18
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ADDRESSES MEDIAES & CARROLL, LIP

STREET: 220 Voltegomery Street, Suite 2200

CITY: San Francisco

CITY: San Francisco

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CONTRETE SEADALE FORM disk

CONTREME SEADALE FORM disk

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CONTREME PARLICATION DATA:

FILMON DATE:

CONTREME PARLICATION DATA:

FILMON DATE:

CONTREME PARLICATION DATA:

APPLICATION NUMBER: US/08/934.097A

TELEPRA: (413) 397-6338

INFORMATION PROBED IN CONTREME

SEQUENCE CHARACTERISTICS:

LENGTH: Passe pairs

SEQUENCE: (413) 397-6338

DESCRIPTION: (4600 = "UNA")

MARCHES J. CONTRETION: (4000 = "UNA")

APPLICATION: AND MASSE CONTRETIONS

NOTICE THE PASSE CONTRETION: (4000 = "UNA")

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CONTRETION: AND MASSES CONTRETION: (4000 = "UNA")

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MARINA TYPE: ADDRESS: (4000 = "UNA")

CONTRETION: (4000 = "UNA")

AND MASSES CONTRETION: (4000 = "UNA"
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CURRENT APPLICATION NUMBER: US/09/380,836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/09677192
| Sequence 48, Application US/09677192
| Patent No. 638691
| GENERAL INFORMATION:
| APPLICANT: Lyamichev, Victor I. APPLICANT: Brow, Mary Ann D. APPLICANT: Pors, Lance
| APPLICANT: Pors, Lance P. APPLICANT: Pors, Lance P. TITLE OF INVENTION: OLIGONUCLEOTIDES | TITLE OF INVENTION: OLIGONUCLEOTION: ONWHER: US/09/677,192 | PRIOR APPLICATION NUMBER: U9/034,205 | PRIOR APPLICATION NUMBER: 09/034,205 | PRIOR APPLICATION NUMBER: 09/034,205 | PRIOR PILING DATE: 1998-03-03 | SOFTWARE: PatentIn Ver. 2.0 | SOFTWARE: PatentIn Ver.
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Batent No. 6551775
GENERAL INFORMATION:
APPLICANT: Lifton, Richard P.
APPLICANT: Lifton, Richard S.
TITLE OF INVENTION: Method to Diagnose and Treat Pathological Conditions
TITLE OF INVENTION: Resulting from Deficient Ion Transport such as
FITLE OF INVENTION: Applications of the Conditions
TITLE OF INVENTION: Resulting from Deficient Ion Transport such as
FITLE REPERENCE: 44574-5018-035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-03268
TELECOWUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPPLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
32.0%; Score 6.4; DB 1;
Best Local Similarity 87.5%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 1.
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US-09-677-192-48/C
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US-09-989-789-2195/c
US-09-989-789-2195/c
Sequence 2195, Application US/09989789
Fatent No. 6589746
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
TITLE OF INVENTION: TRIPLETS BY 211-US2
CURRENT APPLICATION UNMERR: US/09/989, 789
CURRENT APPLICATION UNMERR: 2002-03-03
NUVMBRR OF SEQ ID NOS: 4085
SOFTWARE: PATENTING DATE: 2002-03-03
SEQ ID NO 2195
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Segment of mutant alpha ENAC allele US-09-380-836-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Willem A.
APPLICANT: Haeringen van, Hendrik
TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
TITLE OF INVENTION: 2010-10-03
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: EP 00200757.3
PRIOR APPLICATION NUMBER: PCT/NL01/00177
PRIOR PILING DATE: 2001-03-03
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/040,171
PRIOR FILING DATE: 1997-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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RESULT 178

PCT-1995-01008-2

Sequence 2, Application PC/TUS9601008

Sequence 2, Application PC/TUS9601008

Sequence 2, Application PC/TUS9601008

Sequence 3, Application Formation for APPLICANT: Moreoten Foundation Formation Inhibitors and Methods of Their Use CORPUTED OF SEQUENCES: 20

ADDRESSEE Lappin & Kusmer Street

CITYENT: 05000

STATE: Messachusets

COMPUTER: IBM PC compatible

COMPUTER:
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                                                                TYPE: DNA ORGANISM: Artificial Sequence PETURE: PEATURE: OPHER INFORMATION: Description of Artificial Sequence: primer US-09-958-221A-7
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                                                                                                                                                                                                                                                                                Query Match 32.0%; Score 6.4; DB 1; Length 9; Best Local Similarity 87.5%; Pred. No. 3.6e+02; Matches 7; Conservative 0; Mismatches 1; Indels
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SEQ ID NO 7
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Search completed: June 8, 2004, 12:28:07 Job time : 1 secs IGFBP2 oligonucleo IGFBP2 oligonucleo IGFBP2 oligonucleo IGFBP2 oligonucleo IGFBP2 oligonucleo IGFBP2 oligonucleo

Myeloid progenitor Human N-acetylgala RNA sequence #5, f Left primer DBW011 Human skin EST 919 Human skin EST 176

Random

model 3 using search, nucleic nucleic ĕ June ü Run

8, 2004, 12:25:33 ; Search time 0.001 Seconds (without alignments) 187.440 Million cell updates/sec

US-10-003-919-21 20 Title: Perfect score: Sequence:

1 ATGGACTCGCTGGCACGCAC 20

IDENTITY NUC Gapopt 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

415 seqs, 4686 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 415 summaries

rngdb:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Human Ship-1 antis Primer for adenovi Capture oligonucle Human RECQL2 antis TRADD antisense ol NOTO4 polymorphis PCR primer #2 used Human T125 cDNA am Adaptor directed p Human GDMLP-1 17-m Human GDMLP-1 17-m Mouse p21MPL CCCG Nhel 5' PCR primer Tag sequence of a DB Length % Query Match I 00000000000

AAD61197
AAT33529
AB13529
AAD41745
AAZ93489
AAC98469
AAD61442
AAD612442
AAD612463
AAD727875
AAT27875
AAT27875 AAI71593 AAX09136 AAF45238

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AAF73837 ACD66350 ACD66420

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Primer NGFTE-4 use Alpha2 integrin pr Human fit-1 and XD Human FKBPB allele IGFBP2 oligonucleo Sample preparation Sample preparation Human CETP HH ribo M. avium 16S rRNA Human CETP HH ribo ABV71331 ABV63910 ACA61749 ACA61769 AAT49691 ABX76579 AAT49650 AAI67291 AAF45958

AAF45240 AAF45255 AAF45236 AAF45232 AAF45237 AAF45241 AAF45241 AAF459156 ABT05510 ABS59479

ABV99924 AAD48184 AAD48185 AAD48186 AAZ78944

Oligonucleocide SE Oligonucleocide SE Oligonucleocide SE Oligonucleocide SE FSV RNA fragmucleocide SU Flu-2 PNA probe us Flu-4 PNA probe us Human dendritic ce Human dendritic ce Human McNGNB1 gene p Human skin EST 165 Human skin EST 282 Template sequence Template

ABL52050 ABV63868 ABV71289

CFTR gene analysis Detection probe #D Detection probe #D Positive control 1

AAZ40108 AAZ40248

Nucleotide sequenc Nucleotide sequenc

ABH86576 ABH86514

Oligonucleotide proligonucleotide proligonucleotide proligonucleotide proligonucleotide proligonucleotide proligonucleotide SE Anti-HCV nucleic a 168 xRNA gene frag Human dendritic ce Metastatic breast Metastatic breast

IGFBP2 Oligonucle Human SLC6A4 allel Anti-HCV nucleic a Anti-HCV enzymatic Human skin EST 911 Human skin EST 169

Lambda vector base Human biallelic po rag sequence of a Human pancreatic

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ABQ87015 ABQ86921 ABQ87551

Human monocyte gen Human dendritic ce Human bormal bepat Yeast NORF gene SA Chronic hepatitis Human HCC underexp Human apolipoprote Human apolipoprote Human apolipoprote Human apolipoprote Human apolipoprote Human St. S. -O-alkylamino-co Human skin stress/Human sk

Human skin EST 983 Human skin EST 580 Human skin EST 753 Human skin EST 285 Human skin EST 285 Human skin EST 915 Human skin EST 974 Human skin EST 977 VMCHelic acid analy	Vemplate sequence Human adenosine re Human (CkBP polynu Oligonucleotide pr	oligonucleotide pr Oligonucleotide pr	oligonuclectide proligonuclectide proligonuclectic proliforum prolifo	Human skin EST 419 Human skin EST 886 Human skin EST 886 Human skin EST 885 Human skin EST 332 Human skin EST 534 Human skin EST 534 Human skin EST 534 Human skin EST 307 Human skin EST 307 Human skin EST 995 Human skin EST 995 Human skin EST 995 Human skin EST 883 Trichoderma reesei Herpesvirus inhibi Trichoderma reesei Adapter linker nuc
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AAZI8779 ABQ8766 ABQ87184 ABQ86321184 ABV6828 ABV6428 ABV6428 ABV6405 ABV6405 ABV6405 ABV6405 ABV6405 ABV64105 ABV71705

ABQ71448 ABBC71449 ABBC714449 ABBC71845 ABBC8656 ABBC86566 ABBC84523 ABBC84521 ABBC84521 ABBC84521 ABBC85256 ABBC8523 ABBC8523 ABBC8523

Human ubiquitously
Human ubiquitously
Linker used to mak
Human DRD2 polymor
Ceralloplasmin (fer
Yeast NORF gene SA
Yeast NORF g

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Human; Ship-1; SH2-containing phosphatidylinositol phosphatase-1; INPP5D; insensitivity to apoptotic signal; developmental disorder; inflammation; immunosuppressive; autoimmune disorder; antisense therapy; antisense;
8kin EST 667

8kin EST 326

8kin EST 142

8kin EST 768

8kin EST 768

8kin EST 881

8kin EST 888

8kin EST 528

8kin EST 528

8kin EST 528

8kin EST 528

8kin EST 528
                                                                                                              pGL3 basic vector
DNA tag used to id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense compounds targeted to nucleic acid molecule encoding Ship-1, useful for treating diseases associated with expression of Ship-1, such as autoimmune and developmental disorders.
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                                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidines are methyl cytidines"
Human skin B
                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/mod_base= OTHER
/note= "2'-0-methoxyethyl (2'-MOB) nucleotides"
16. .20
                                                                                                                                                                                                                                                                                                                                                                                                     'note= "2'-0-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                            Human Ship-1 antisense oligonucleotide ISIS #168278.
                                                                                                                                            ALIGNMENTS
                      ABV63636
ABV67898
ABV69888
ABV69088
ABV67499
ABV67499
ABV67449
ABV62437
ABV63211
ABV63211
ABV63211
ABV63211
ABV63211
ABV63211
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                phosphorôthioate backbone; ss.
                                                                                                                                                                                 AAD61197 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2001; 2001US-00003919.
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                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Freier SM;
  (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-801302/75.
 US2003114401-A1
                                                                                                                                                                                                                                                                                                       Key
modified_base
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                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
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 AAD61197;
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AAT3329-30 are primers used to determine the absence of adenovirus Ela nucleotide sequences in an adenoviral (Adv) vector encoding for the captression of human wild-type p53 protein (Adw1p53). New Adenoviral (Adv) extors comprise: (i) an oxigin of replication; (ii) a left inverted terminal repeat; (iii) a nucleotide sequence of the Adv genome contg. Clai sites, one at the 5'-and; and (iv) a homologous recombination comain. Adv vectors which also contain heterologous DNA and regulatory sequences, are used to inhibit cell proliferation (including abnormal vascularisation), esp. to treat human melanoma, breast or lung tumours, are also used to treat human melanoma, breast or lung tumours carcoma and carcinoma, including forms resistant to drugs. The vectors are also used to treat subjects at risk of such cancers, and to purge are also used to treat subjects at risk of such cancers, and to purge the second (upstream) Clai site greatly reduces the chance of production of the second (upstream) Clai site greatly reduces the chance of producing Undingested DNA genome and increases the chance of generating fully cut DNA (i.e. redu. of parental genomic based vector; and infect breast
                                                                                                                                                                                                                                                                                          ö
                                    The present invention provides antisense compounds targetted to nucleic acid molecule encoding Ship-1 (also Known as SH2-containing phosphatidylinositol phosphatae-1 and INPPED) to modulate/Anhibit the expression of Ship-1. The invention is useful in treatment of diseases such as insensitivity to apoptotic signals, autoimmune disorders, developmental disorders and inflammatory disorders. The present sequence is human Ship-1 antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno:viral vector for gene therapy of cancer or bone marrow purging contains two ClaI restriction sites to increase chance of generating fully cut DNA, thus reducing the parental genomic background.
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer; polymerase chain reaction; PCR; adenoviral vector; p53; Ela;
wild-type; inhibit; cell proliferation; melanoma; breast tumour; ss.
                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                           Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer for adenovirus Ela nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                              Arceacrectedeacecae 20
                                                                                                                                                                                                                                                                                                                                          1 ATGGACTCGCTGGCACGCAC 20
Claim 3; Page 24; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
AAT33529/c
ID AAT33529 standard; DNA; 20 BP.
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Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA ampilification, replication, recombination or repair, the cancer is specifically associated with a gene selected from BRCA1 gene, buman papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food method is also used for environmental monitoring, forensics and the food electron microscope and infrared microscope) the support at the food particular sites and identifying if ligation of the oligonucleotide probe sets occurred and correlating (using a computer) identified ligation to a presence or absence of the target nucleotide sequences. ABI82074 to
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                                                                                                                                                                                                                                                                                                                                      Human, K-ras, PCR primer, probe, capture probe, mutation detection, ligase detection reaction; LDR, p53; BRCA1, BRCA2, infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer, oncogene, tumour suppressor; human papillomavirus; forensic; environmental monitoring; food industry; feed industry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Designing capture oligonucleotide probes for use on a support to which complementary oligonucleotides hybridize with little mismatch.
                                                                                    Gaps
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0
                                                   Score 13.4; DB 1; Length 20;
Pred, No. 11;
                                                                                    Indels
cancer cells far more efficiently than bone marrow cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kliman R;
                         Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           Capture oligonucleptide Zip ID#15 oligo #9.
                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 29; 300pp; English.
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                                                                                                                                                                                 RESULT 3
AB192928/c
1D AB192928 standard; DNA; 20 BP.
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                                                      Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                  5 ACTCGCTGGCACGCA 19
                                                                                                                                             18 Acrederedeacrea 4
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                                                             Gaps
                                                                                                                                                                                                                                                                                                                             Antisense, RECQL2, Bloom's disorder; prophylaxis; infection; tumour; inflammation; therapy; human; phosphorothicate; ss.
                                                             .;
0
                            Score 13.4; DB 1; Length 20;
Pred. No. 11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                  Human RECQL2 antisense oligonucleotide, ISIS #137525.
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*t.aga= b
*mod_base= OTHER
*note= "2'-methoxyethyl nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      '*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone"
Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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mod base= OTHER
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/mod_base= m5c
15..17
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16. .20
/*tp:
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/mod_base= m5c
7..\overline{8}
                                                                                                                                                                  RESULT 4
AAD41745/c
ID AAD41745 standard; DNA; 20 BP.
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/mod_base= m5c
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                             Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001; 2001US-00798096.
                                                                                             6 CTCGCTGGCACGCAC 20
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                                                                                                                                                                                                                                                                     (first entry)
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                     AAD41745;
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/note= "Complementary to bases 811-794 of the human TRADD
sequence described in GENESEQ record AAZ93431"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense compounds that limit the expression of human TRADD protein, useful in the treatment and diagnosis of cancer, inflammation and septic
                                                                                The invention relates to antisense compounds targetted to nucleic acid encoding RECQL2 (gene associated with Bloom's disorder) to inhibit the expression of RECQL2. Antisense compounds of the invention are useful for treating diseases associated with expression of RECQL2, in humans. They are useful for diagnostics, therapeutics and as research reagent, e.g. prophylactically to prevent or delay infection, inflammation or tumour formation. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human RECQL2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The intracellular protein TRADD has been identified as a critical link between tumour necrosis factor (TNF) receptor binding and downstream activation of NF-kappa-B. Overexpression of native TRADD activates NF-Kappa-B in the absence of TNF and dominant negative mutants of TRADD block TNF-induced NF-kappa-B activation. A second effect of TNF in many cell types is the induction of apoptosis (programmed cell death). TRADD
with Bloom's disorder, for modulating RECQL2 expression and treating diseases e.g. tumors associated with expression of the RECQL2 in humans.
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRADD, TNF, tumour necrosis factor, NF-kappa-B, apoptosis, programmed cell death, antisense, inhibition, treatment, therapy, septic shock, inflammation, cancer, antiinflammatory, human, ss.
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                                                                                                                                                                                                                                                                          DB 1; Length 20;
                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                         Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        66.0%; Score 13.2; D:
83.3%; Pred. No. 12;
ative 0; Mismatches
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                                                    Example 15; Col 44; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRADD antisense oligonucleotide.
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                                                                                                                                                                                                                                                                                                                                               2 TGGACTCGCTGGCACGCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                            Local Similarity 83.3
nes 15; Conservative
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misc_binding
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overexpression has been shown to mimic TNP induction of apoptosis as are the rate limiting step of TTR action and would therefore serve as the most efficient targets for inhibition of TNF-induced events. Antisense oligonucleotides capable of inhibiting TNPD function may therefore be useful in a number of therepetic, diagnostic and research applications. Inhibiting expression of TRADD by contacting human cells or tissues with the antisense compound may be used to treat a disease or condition associated with TRADD expression, for example, septic shock, inflammation, or cancer. TRADD antisense oligonucleotides of varying finhibitory capabilities are listed in GENESEQ records AAZ93438-Z93517. The antisense oligonucleotides exhibit enhanced inhibitory capabilities when they have 2'-MOE wings and a deoxy gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining whether an individual is predisposed to susceptibility to low bone mineral density (BMD) and/or bone damage, involves identifying polymorphisms in associated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             low bone mineral density, BMD; bone damage; polymorphism; osteoporosis; single nucleotide polymorphism; SNP; PCR primer; ss; human.
                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                         65.0%; Score 13; DB 1; Length 18; 100.0%; Pred. No. 13; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOT304 polymorphism marker PCR primer B primer seq.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC98469 standard; DNA; 16
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                                                                                                                                                                                                                                                                                                                                                                                           2 TGGACTCGCTGGC 14
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Les 13; Conservative
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I, Schafer A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC98469;
                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
ADC98469
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Human; haematopoiesis; clotting; kidney failure; wound healing; cancer; neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease; neart disorder; ischaemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive; glomerular disease; glomerulonephritis; uterine disorder; hyperplasia; fetal spleen; prostate disorder; inflammatory disease; Crohn's disease; proliferative disorder; gynaecological; haemostatic; antibacterial; systemic lupus erythematosus; immunodeficiancy disorder; antibacterial; officeratic; nephrotropic; antidabetic; cerebroprotective; tranquilliser; hypotensive; tumnur; injury; trauma; antidandal; vasotropic; antiulcer; apoptotic disorder; heumatoid arthritis; cardiant; renal disorder; hepatotropic; antipleoriatic; dermatological; virucide; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to nucleic acids encoding a variety of proteins human T139 (TRANGO-110), wurnine T175 (TRANGO-110), wurnine T175 (TRANGO-175), human T175 or marine WDMM-2, having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability,
                                                                                                                                                                                                                      Gaps
low {\rm BMD} and/or bone damage is osteoporosis. The present PCR primer sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer #2 used to analyse the distribution of human T125 mRNA.
                                                                                                                                                                                                                         ö
                                                                                                                                                       DB 1; Length 16;
20;
                                                                                                                                                                                                                   0; Indels
                                                                                            Sequence 16 BP; 2 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                       Score 12; DB pred. No. 20; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodearl ADJ, Mccarthy SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 42; 138pp; English.
                                                                                                                                                       60.0%; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD33544 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00065363.
98US-00102705.
98US-00124538.
99US-00238531.
99US-00337930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                         TGGACTCGCTGG 12
                                                                                                                                                                                                                                                                                 2 TGGACTCGCTGG 13
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GOODEARL A D J.
MCCARTHY S A.
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22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-1999
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer; ss.
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ID AAD33544/C
XX AAD3355
XX AAD3355
XX AAD3355
XW Human;
XW Human;
XW Human;
XW Human;
XW Glomen;
XW C Glom
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to inhibit a proteinase activity, to modulate cell-cell interactions, haematopoiesis and the ability to modulate clotting. Polypeptide and properties and the ability to modulate clotting. Polypeptide and control of discrete characterised by their aberrant expression or activity. The discrete characterised by their aberrant expression or activity. The antibodies are useful as modulating agents in regulating a variety of callular processes e.g. cell proliferation and/or cell differentiation. TANGO-139 is useful in wound healing and for treating cancer, TANGO-110 is useful in wound healing and for treating cancer, TANGO-110 is useful for treating neoplasia, TANGO-17 or WDNM-2 is useful for treating cancer, are useful to treat pancreatid disorders, such as pancreatids. TANGO-125, 110, 175 molecules treat heart disorders, e.g., the brain. TANGO-125, 110 and 175 molecules are useful for treating cancer, are disorders, such as glomerular disease (e.g., acute and chronic glomerulonephritis), TANGO-175 is useful to treat uterine disorders, such as glomerular diseases eru uterine disorders, such as glomerular diseases and sorder. TANGO-175 is useful to treat uterine cylence, e.g., the fetal spleen, associated diseases and disorders, such as inflammatory disorders. TANGO-185, 125, 110, 175 or WDNM-2 are useful for treating proliferative disorders, such as inflammatory disorders. TANGO-185, systemic lupus erythematosus, insulin-dependent dispetes mellitus, immune related disorders, e.g., insulin-dependent dispetes mellitus, immune related disorders, e.g., insulin-dependent dispetes mellitus, immune related disorders, e.g., insulin-dependent disorders, org., insulin-dependent disorders and context and disorders, e.g., insulin-dependent disorders and Human; TANGO; kidney failure; hyperplasia; inflammatory disorder; cancer; angiogenesis; hematopoietic disorder; pancreatic disorder; bearcreatic disorder; bearcreatic disorder; testicular disorder; proliferative disorder; tumour; ovulation disorder; testicular disorder; lung disorder; Crohn's disease; prostate disorder; Mipple's disease; hemophiliser; vulnerary; vasotropic; psoriasis; leukaemia; gene therapy; tranquillizer; vulnerary; vasotropic; psoriasis; leukaemia; daundice; immunosuppressive; abortion; ischaemia; arthritis; allergy; Gaps ö 59.0%; Score 11.8; DB 1; Length 18; 86.7%; Pred. No. 24; 21; o. Mismatches 2; Indels Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 U; 0 Other; Human T125 cDNA amplifying PCR primer #2. 23-APR-1998; 98US-00065661. 23-APR-1999; 99US-00298531. 21-FEB-2001; 2001US-00790264. 11-OCT-2002; 2002US-00269353. 2 TGGACTCGCTGGCAC 16 17 redectréceasécac 3 AAD61442 standard; DNA; 18 (first entry) Local Similarity 86.7 1es 13; Conservative PCR; primer; ss. US2003104447-A1. Homo sapiens. 15-JAN-2004 05-JUN-2003, AAD61442; Query Match asthma; AAD61442/c Matches RESULT 8 8595959595959595959595959595 ઠે

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The invention relates to an isolated polypeptide termed human T139 (TANGO 139), T125, T110, musine T175, human T175 or musine NDMP-2 T139 is useful for treating kidney defects such as kidney failure or hyperplasis useful for treating wound healing and cancer, T110 is useful for treating explanata, inappropriate andiogenesis or tissue regeneration and hammare trains neoplasis. T125 and 110 are useful to treat pancreatid chaematopoietic disorders. T125 and 110 are useful to treat pancreatid disorders such as pancreatidis, diabetes mellitus, and Zollinger-Ellison sinceres placental disorders such as placentitis or abortion and disorders of the brain such as retering and control in such as cerebral edema, cerebrovascular disease and tumours and injury or tramma to the brain. T125, 110, 175 molecules of the brain such as mecular y disorders such as receptal and disorders such as mecular disorders such as required to some such as mecular disorders including jaundice, hepatic fallure, Crigler-Naijar syndromes or including jaundice, hepatic janud 175 seventerion and ovarian disorders such as glomerular disorders including content and falsorders such as glomerular disorders, hypothasia of the endometrium, uterine cancer, bone marrow, blood and haematopoid et or disorders such as disorders such as originated diseases and disorders end, sorders such as originated and the falsor such as originated and sorder such as originated and sorder such as ori
                                                                                                                                                            New TANGO polypeptides useful as modulating agents in regulating cellular processes and for diagnosing, treating heart, liver, lung, kidney, inflammatory and cellular proliferative disorders.
                                                                      Mccarthy SA;
                                                                                                                                                                                                                                                            Example 6; Page 42; Opp; English
                      (MILL-) MILLENNIUM PHARM INC.
                                                                      Goodearl ADJ,
                                                                                                                 WPI; 2003-787050/74.
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Gaps
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0
                              DB 1; Length 18;
                                                             2; Indels
Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
                            Score 11.8; DE
Pred. No. 24;
0; Mismatches
                              Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                           2 TGGACTCGCTGGCAC 16
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AAT27875 standard; DNA; 17 BP
reeccreecaecae
                                   AAT27875/C

ID AAT27878'

XX AAT278'

XX DT 27-JAN-

XX Adaptor
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Adaptor directed primer Hnd.pr.4. (first entry) 27-JAN-1997

AAT27875;

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Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect opd. simple sequence repeat, and an adaptor segment. The present sequence is expensed to an adaptor segment. The present sequence is an example of an ADP, which spans the length of, and is complementary to, one strand of a double stranded adaptor that is ligated into the restriction endouclease digested target DNA. It therefore covers all or part of the restriction site, and its 3 end can carry arbitrary, non-degenerate bases that anneal to, and prime from nucleotides within the target DNA fragment adjacent to the adaptor. The method represents a modified amplified fragment length polymorphism assay, which is partic, useful for genome fingerprinting, i.e. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.
               Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed priner; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; ss.
                                                                                                                                                                                                                /note= "arbitrary non-degenerate bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic trait marking and germplasm comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                 (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                    Location/Qualifiers
15. .17
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 35; 173pp; English
                                                                                                                                                                                                                                                                                                                                      95WO-US015150
                                                                                                                                                                                                                                                                                                                                                                            94US-00346456
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morgante M, Vogel JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPI; 1996-277795/28.
                                                                                                                                                                                                                                                                                                                                                                            28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                      21-NOV-1995;
                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                        409617082-A2
                                                                                                                 Synthetic
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Score 11.2; DB 1; Length 17; Pred. No. 32; 0; Mismatches 3; Indels ABN09923 standard; DNA; 17 BP. Query Match
Best Local Similarity 81.2%;
Matches 13; Conservative 4 GACTCGCTGGCACGCA 19 N 17 GACAAGCTGGTACGCA (first entry) 29-MAY-2002 ABN09923; ABNO9923/C XX ABNO XX ABNO XX ABNO XX ABNO XX W Hume XX W Hume XW Muse KW Muse KW Muse KW Muse KW Muse 엄

Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9915.

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Gaps

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 claim be used an gene therapy and vaccine production. The hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phonotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodiaes that specifically recognise hGDMLP-1 proteins, as specific biomolecule capture probes for surface-enhanced laser description ionisation, and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser description ionisation, as production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence in the exemplification of the present invention. N.B. The sequence date for this patent did not form part of the printed specificalion, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 9915; 214pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                          2001WO-US000663.
2001WO-US000664.
2001WO-US000665.
                                                                                                                                                                                                                                                                                                                                 2001WO-US000666.
                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
                                                                                                                              25-MAY-2001; 2001WO-US016981
                                                                                                                                                                                                                         2000GB-00024263
                                                                                                                                                                                                                                           2001WO-US000661
2001WO-US000662
                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2001; 2001US-0266860P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AEOM-) AEOMICA INC.
                                                     WO200192524-A2
                                                                                                                                                                                                                                                                          30-JAN-2001; 2
30-JAN-2001; 3
30-JAN-2001; 2
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                   Homo sapiens,
                                                                                                                                                                                                                                           30-JAN-2001;
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                                                                                        06-DEC-2001
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Shannon ME;

Chen W,

Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Gaps . 0 56.0%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 32; tive 0; Mismatches 3; Indels Local Similarity 81.2 les 13; Conservative Query Match Best Loca Matches

; 0

1 ATGGACTCGCTGGCAC 16

AGGACTCGCAGGAAC

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RESULT 11 ABN09922/c

ABN09922 standard; DNA; 17 BP

(first entry)

29-MAY-2002

Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9914.

Human, genome-derived myosin-like protein 1, GDMLP-1, hGDMLP-1, heart, muscle, myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

Homo sapiens

WO200192524-A2.

06-DEC-2001

25-MAY-2001; 2001WO-US016981

2001WO-US000662 2001WO-US000663 2001WO-US000664 2001WO-US000661 30-JAN-2001 30-JAN-2001 30-JAN-2001 30-JAN-2001 30-JAN-2001 30-JAN-2001 30-JAN-2001 30-JAN-2001

; 2001WO-US000668. ; 2001WO-US000669. ; 2001WO-US000670. ; 2001US-0266860P. 2001WO-US000665 2001WO-US000666 2001WO-US000667 30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

(AEOM-) AEOMICA INC.

05-FEB-2001;

WPI; 2002-179446/23.

Shannon ME; Chen W, Hanzel DK, Rank DR, Gu Y, Ji Y, Penn SG, New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.

Disclosure; SEQ ID NO 9914; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 clambe used as probes to detect, characterise and quantify nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phonotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be protein variants having desired phonotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specific biomolecule add/or amount specifically of hGDMLP proteins, as specific biomolecule and/or amount specifically recognise hGDMLP-1 and/or amount specifically recognise hGDMLP-1 capture probes for surface-enhanced laser describing in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The production and with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders, hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hospital muscle dates for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. at ftp.wipo.int/pub/published_pct_sequence

Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

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                        Gaps
                      ö
   Length 17;
                      3; Indels
Score 11.2; DB 1;
Pred. No. 32;
0; Mismatches 3;
                      ;
0
  56.0%;
81.2%;
                        13; Conservative
 Query Match
Best Local Similarity
Matches 13; Conserv
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AAD27555 standard; DNA; 11 BP.

AAD27555;

18-APR-2002 (first entry)

Mouse p21WAF1 CCCGGG motif 5' flanking DNA.

p53 protein; pGL3 luciferase reporter vector; luc+; transcription factor; cell cycle control; DNA damage repair; apoptosis; mouse; p21WAF1 DNA; ds.

Mus sp.

WO200196602-A2.

20-DEC-2001.

18-JUN-2001; 2001WO-GB002718

16-JUN-2000; 2000GB-00014820.

(MEDI-) MEDICAL RES COUNCIL.

Yang AL, Festing M;

WPI; 2002-130743/17.

Determining the p53 status of a sample, useful for assaying for mimetics or antagonists of p53, or for the presence of DNA damage, comprises determining whether p53 binds to the pGL3 vector in a sample containing a pGL3 vector.

Disclosure; Page 12; 53pp; English.

The patent discloses methods for determining the p53 status of a sample which comprise providing a sample containing a pGL3 luciferase reporter vector and determining whether p53 binds to the pGL3 uciferase reporter transcription factor that regulates many genes including those associated with cell cycle control, apoptosis and DNA damage repair. pGL3 reporter vectors contain a modified firefly luciferase cDNA designated luci, p53 protein binds to pGL3-basic vector and causes luciferase expression. The method is useful for determining the p53 status of a sample. It is also useful for assaying for minetics or antagonists of p53 and for assaying for presence of activated p53 and/or DNA damage. The invention also relates to a method of modifying pGL3 vector which involves deletion or alteration of a CCGGGG motif of the pGL3 vector and/or caleting or alteration of a CCGGGG motif of the pGL3 vector and/or deleting or alteration as sequence within 20 bp sequence 5 or 3 of CCGGG motif. The nucleic acid having a sequence incorporating the CCGGG motif is useful for conferring promoter activity or p53-responsiveness on a nucleic acid activity. The present DNA sequence is mouse p21MAFI CCGGGG motif is conferred to the present DNA sequence is mouse p21MAFI CCGGGG motif to confer promoter activity. This sequence is used along with CCGGG motif to confer flanking DNA. Thi promoter activity RESULT 12
AAD27555/C
AAD27555/C
AAD27555/C
AAD27555/C
AAD27555/C
AAD27555/C
AAD27
AAD

Seguence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Gaps . 0 55.0%; Score 11; DB 1; Length 11; 100.0%; Pred. No. 25; o; Indels iive 0; Mismatches 0; Indels 11; Conservative Query Match Best Local Similarity Matches

11 GACTCGCTGGC

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ABL91653 RESULT

BP. ABL91653 standard; DNA; 12

ABL91653;

(first entry) 29-JUL-2002 Nhel 5' PCR primer tail used in Chlamydia pneumoniae gene amplification.

Chlamydia pneumoniae; chlamydial infection; antigen; immunogen; vaccdiagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; calaudication; stroke; strain (MADO29; open reading frame; ORF; Escherichia coli; recombinant expression; primer tail sequence; PCR;

primer; ss Synthetic. WO200202606-A2.

10-JAN-2002.

03-JUL-2001; 2001WO-IB001445

03-JUL-2000; 2000GB-00016363.

11-JUL-2000; 2000GB-00017047. 21-JUL-2000; 2000GB-00017983. 07-AUG-2000; 2000GB-00019368. 18-AUG-2000; 2000GB-00020440.

14-SEP-2000; 2000GB-00022583. 10-NOV-2000; 2000GB-00027549. 22-DEC-2000; 2000GB-00031706.

(CHIR-) CHIRON SPA.

Ratti G, Grandi G;

WPI; 2002-154726/20.

Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes.

Example, Page 33, 364pp; English

Dequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as therosclerosis, coronary artery disease, carcoid artery stenosis, coronary artery disease, acroid artery stenosis, myocardial infarction, cerebrovascular disease, acrtic aneurysm, cliantocation and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the proteins and mucleic acids of the invention prevention or treatment of chlamydial infections, particularly Chlamydia prevention or treatment of chlamydial infections, particularly Chlamydia (Chlamydia pneumoniae, and the notleic acids may also be used in the defection of Chlamydia pneumoniae, and the notleic acids may be used in the Sequences of Sequences ABL91182-ABL91657 represent PCR pneumoniae gene expression of sequences ABL91182-ABL91657 represent PCR primer tail sequences containing restriction enzyme sites used in the exemplifications in the amplification of the novel Chlamydia pneumoniae containing restriction enzyme sites used in the exemplifications in the amplification of the novel Chlamydia pneumoniae

Sequence 12 BP; 1 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match

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DB 1; Length 12; 52.0%; Score 10.4;

4 GACTCGCTGGC 14

Matches

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RESULT 14

AAX31582

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The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer SAGE tags of the invention
                                                                                      colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; analysis of gene expression; diagnostic; prognostic; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lambda vector; cloning system; homologous recombination; eukaryote; embryonal stem cell; adaptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human nucleic acid containing specific SAGE tags, useful as
diagnostic markers for cancer, also derived probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
52.0%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 45;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lambda vector based cloning system adaptor sequence Sfi-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 2 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                    Zhou W;
                                                    Human pancreatic cancer SAGE tag #88
                                                                                                                                                                                                                                                                                                                                                                                    Zhang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Col 73; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                          98US-00081646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI71593 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                    Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0-JAN-2002 (first entry)
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                                                                                                                             marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                    Vogelstein B,
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                                                                                                                                                                                                                                                                        20-MAY-1998;
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                                                                                                                                                                Homo sapiens
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                                                                                                                               cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentially expresent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or no both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comprises comparing the level of at least one transcript in a first sample of a tissue to a being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX10947-31815. The methods of the invention can be used in the diagnosis, prognosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of isolated gene transcripts - useful for developing products for diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.
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                     Gaps
                                                                                                                                                                                                                                                                                                                            Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss.
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                     Indels
                       1;
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   Pred. No. 38;
0; Mismatches
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                                                                                                                                                                                 AAX31582 standard; DNA; 15 BP.
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91.78;
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ses 11; Conservative
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                     11; Conservative
                                                    9 GCTGGCACGCAC 20
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                                                                                      12 GCTAGCACGCAC 1
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 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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RESULT 15

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The present invention describes a cloning system useful for homologous recombination in eukaryotic cells and consisting of a vector-adaptor system with a lambda vector and 4 adaptor nucleotides. This can be used to alter the genome of eukaryotic cells, particularly embryonal stem cells, at a desired location. The present sequence is an adaptor sequence used in the construction of the lambda vector of the invention AAX09121-X10268 are allele-specific oligonucleotide primers used in the isolation of various biallelic polymorphic markers found in the human genome (represented in AAX10269-X12937). These primers can be used in a method for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular Cloning system for homologous recombination, useful for introducing mutations into eukaryotic genomes at selected sites, comprises lambda Polymorphism, biallelic, human, forensic, paternity testing, disease, detection, phenotypic typing, characteristic, infection, hereditary, autoimmune disease, cancer, inflammation, drug, therapy, medicament, treatment, marker, primer, ss. New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease. Human biallelic polymorphic marker upstream primer #16. Sequence 16 BP; 3 A; 6 C; 7 G; 0 T; 0 U; 0 Other; (WHED) WHITEHEAD INST BIOMEDICAL Claim 15; Page 48; 310pp; English. Disclosure; Page 4; 11pp; German. 52.0%; 91.7%; 97WO-US020313 96US-0030455P AAX09136 standard; DNA; 15 (first entry) Best Local Similarity 91.7 Matches 11; Conservative 3 GGACTCGCTGGC 14 16 GGCCTCGCTGGC 5 Wang D, vector and adaptors. WPI; 1998-286974/25. Wattler S; WPI; 2001-657561/76 Ното варіелв 05-NOV-1997; 06-NOV-1996; WO9820165-A2 24-MAR-1999 14-MAY-1998 Lander ES, Synthetic AAX09136; Query Match Nehls M, RESULT 17 AAX09136 à

Вр. С

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBD3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic; cytostatic; dermatological; cardiant; virucide; opthhalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; plaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatosis; neoplasia; seleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; necovascular condition of the retina; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, tamilial hypercholesterolemia, polycystic Kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary haemorrhagic telangiectasia, familial colonic polyposis, Bhlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obssity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                               DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                       Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                             51.0%; Score 10.2; I
80.0%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                   prophylaxis of such diseases
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                                                                                                                                                                                                                                                                                                                                                                             2 TGGACTCGCTGGCAC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGFBP2 oligonucleotide #77.
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Score 10.4; DB 1; Length 16; Pred. No. 47; 0; Mismatches 1; Indels

1 GGAGTTGCTGGCAAG 15

ACD66350 ACD66350;

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ACD66350 RESULT

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The present invention relates to a polymorphic variant of a reference sequence for the solute carrier family 6 neurotransmitter transporter, seroconin member 4 (SLC6A4) gene or a fragment of it or a sequence complementary to the first sequence. The invention is used in producing a recombinant organism that can be used to express SLC6A4 for protein structure analysis and binding studies. A composition comprising a genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
oligonuclectides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, plantis, serborhoea, keloids, keratosis, neoplasis, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, hard nor skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperpoliferation of the inside of blood vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 gene for identifying drugs for treating disorders related to expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solute carrier family 6 neurotransmiter transporter; seotonin 4; SLC6A4; genotyping; allele specific oligonucleotide; ss.
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                                                                                                                                                                                 Match 51.0%; Score 10.2; DB 1; Length 15; Local Similarity 80.0%; Pred, No. 50; es 12; Conservative 0; Mismatches 1....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human SLC6A4 allele-specific oligonucleotide probe #19
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                                                                                                                                                              Seguence 15 BP; 0 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nandabalan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 19; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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Best Local Similarity 80.09
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                                                                                                                                                                                                                                                                        6 CTCGCTGGCACGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-123317/13
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Matches
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, inozymes, ambezzymes, as hammerhead ribozymes. DNAzymes, inozymes, zinzymes, ambezzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and apteners that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV general modulate the expression and/or replication of HCV. The compounds that modulate the expression and/or replication of HCV. The compounds compounds and methods of the invention are useful for the treatment of degenerative and methods of the invention are useful for the treatment of degenerative and expression such as cirrhosis, liver failure, and hepatocellular expressions. The present sequence represents a target for one of the anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection.
                                                                                       Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus, HBV; RNA stability, RNA expression, RNA synthesis, antisense; enzymatic nucleic acid, hammeribad ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; anti-HCV; viral replication; degenerative, disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; target; ss.
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                                                             Anti-HCV nucleic acid molecule target sequence #233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 322; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2001, 2001US-00817879.
08-JUN-2001, 2001US-00874748.
08-JUN-2001, 2001US-0296876P.
24-OCT-2001, 2001US-0335059P.
                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002; 2002WO-US009187.
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                              (first entry)
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Roberts E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLATT L.
MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-229207/22
                                                                                                                                                                                                                                                     Hepatitis C virus.
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DRAPER K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAVCO P.
                                                                                                                                                                                                                                                                                       WO200281494-A1.
                              23-SEP-2003
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Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BLAT/)
(MACE/)
(MCSW/)
(MORR/)
(PAVC/)
(LEEP/)
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Gaps

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51.0%; Score 10.2; DB 1; Length 15; 80.0%; Pred. No. 50; ive 0; Mismatches 3; Indels

3 GGACTCGCTGGCACG 17

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; harmerhead tibozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; anti-HV; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
                                                                                                                  Gaps
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  HCV nucleic acid molecules disclosed in the present invention
                                                                             DB 1; Length 15;
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                                                                                                                3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             Anti-HCV enzymatic nucleic acid substrate sequence #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morrissey D,
                                     Sequence 15 BP; 2 A; 5 C; 5 G; 0 T; 3 U; 0 Other;
                                                                        Score 10.2; DB
Pred. No. 50;
1; Mismatches
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08-JUN-2001; 2001US-0296876F.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
                                                                          51.0%;
73.3%;
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BLATT L.
MACEGAK D.
MCSWIGGEN J.
MORRISSEY D.
PAVCO P.
                                                                                                                                                                            1 GACUCGUAGGCUCGC 15
                                                                                                                                                     4 GACTCGCTGGCACGC 18
                                                                                                                                                                                                                                                                                             ACD66420 standard; RNA; 15
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                                                                                           Local Similarity 73.3
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Roberts E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus
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DRAPER
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                                                                        Query Match
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(BLAT/)
(MACE/)
(MCSW/)
(MORR/)
(PAVC/)
(LEEP/)
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transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the anti-HCV enzymatic nucleic acid sequences disclosed in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analytss of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or ichthyosis; apositically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGB; neurodermatitis; psoriasis, dermatitis, skin cancer, EST; expressed sequence tag; ss.
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Pred. No. 50;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 51.0%; Sc. Local Similarity 73.3%; Pries 11; Conservative 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HENK ) HENKEL KGAA
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ABV63910;

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Sample preparation and multiplex detection apparatus DNA #9.
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ACA61749 standard; DNA; 12 BP
                                                                                                                                                                                                                                                                                                           98US-00217472.
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                                                                  (first entry)
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nes 10; Conservative
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                                                                  20-AUG-2003
                                                                                                                                                                       Unidentified
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(MI) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Pred. No. 44;
0; Mismatches 0; Indels
                                 Score 10; DB 1; Length 11;
Pred. No. 44;
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Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                          ABV63910 standard; cDNA; 11 BP.
                                  50.0%; S
100.0%;
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Best Local Similarity 100.
Matches 10; Conservative
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                                 Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
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RESULT 23
ABV63910
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RESULT 24 ACA61749

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The invention relates to an apparatus for carrying out sample preparation
and multiplex detection of panels of target nucleic acids and antigens in
a sample, comprising a sample preparation zone, several three dimensional
capture probe platforms for capturing specific classes of target
molecules and spacer elements for separating the sets of three
capture probe platforms. The apparatus is useful for carrying
out multiplex detection of panels of target nucleic acids and antigens of unterest, treating the sample with a sample buffer to form a
pre-processed sample, passing the pre-processes sample buffer to form a
probes of the apparatus, reacting a label with a signal probe, the signal
probe having specificity for at least one other signal probe that is
specific for the target and detecting the reacted level. Sequences
ACAG1741-ACASISO and ACD17023-ACD17041 represent DNA molecules used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Multiplex detection; ss; spacer element; three dimensional capture probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            panels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apparatus for carrying out sample preparation and detection of panels target nucleic acids and antigens in a sample, has sample preparation zone, three dimensional capture probe platforms and spacer elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 47; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 12 BP; 2 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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Tue Jun

98US-00217472.

95WO-US016000

11-DEC-1995;

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The invention relates to an apparatus for carrying out sample preparation and multiplex detection of panels of target nucleic acids and antigens in a sample, comparising a sample preparation zone, several three dimensional capture probe platforms for capturing specific classes of target molecules and spacer elements for separating the sets of three dimensional capture probe platforms. The apparatus is useful for carrying cut multiplex detection of panels of target mucleic acids and antigens of antigens of interest, treating the sample with a sample buffer to form a processed sample passing the pre-processes sample buffer to form a proparatus, capturing the target nucleic acids and antigens of the apparatus, reacting a label with a signal probe that is probe having specificity for at least one other signal probe that is specific for the target and detecting the reacted level. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage; neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia; peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor; angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
                                                                                                                                                                                                                                                      Apparatus for carrying out sample preparation and detection of panels of target nucleic acids and antigens in a sample, has sample preparation zone, three dimensional capture probe platforms and spacer elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 3 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CETP HH ribozyme target sequence #996.
                                                                                                                                                                                                                                                                                                                               Disclosure; Page 19; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT49691 standard; RNA; 15 BP
                                                                                12-MAR-2002; 2002US-00096718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 TGGCACGCAC 2
                                                                                                                                                                                                                          WPI; 2003-466222/44
                                                                                                                                                   (NANO-) NANOGEN INC
                US2003032029-A1
                                                                                                                   21-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-1997
                                                13-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT49691;
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AAT49608-T49863 represent target sequences for the human cholesterol cester transfer procein (CETP) hammerhead (HH) ribozymes (see AAT498B1-CETP is a 74 kD glycoprotein Lat facilitates neutral lipid transfer between plasma lipoproteins. The numbering of the targets refers to the position of the cleavage site in full length CETP. The ribozyme cc to the position of the cleavage site in full length CETP. The ribozyme is immediately upstream. The ribozymes are able to cleave mRNA from the cgene encoding CETP, thereby blocking synthesis and/or expression of the mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway cc can be inhibited (or eliminated) thereby preventing the reduction in size cenditions associated with ahormal levels of CETP, specifically familial complications associated with ahormal levels of CETP, specifically familial hypercholesterolaemia, atherosclerosis, peripheral vascular disease, hyperbetalipoproteinaemia, atherosclerosis, peripheral vascular disease, to angloplastic restenosis. By inhibiting CETP, the levels of HDL and low density lipoproteins (IDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels).

CT density lipoproteins (IDL), and the HDL:LDL ratio are favourably altered angloplastic restenosis. By inhibiting CETP, the levels of HDL evels).

CT he HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes trains of the CETP gene, they have low non-specific activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe, 23S rRNA, 16SrRNA, tuberculosis; MTC; MOTT; peptide nucleic acid; mycobacterium tuberculosis complex; precursor rRNA; rDNA; 5S rRNA; 8S; mycobacterium other than tuberculosis; mutant; 16S-mediated streptomycin resistance.
                                                                                                                                                                                                                 New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                      Pape
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                                                                                                                                      Couture L, Stinchcomb D, Mcswiggen J, Bisgaler C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 1 A; 7 C; 3 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. avium 16S rRNA mutated probe #8.
                                                                                                                                                                                                                                                                                                       Claim 4; Page 30; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                   94US-00363240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.vv,
Best Local 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX76579 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                             (RIBO-) RIBOZYME PHARM (WARN ) WARNER LAMBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S ACTCGCTGGC 14
                                                                                                                                                                         WPI; 1996-321852/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specific activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS2002137035-A1
                                   23-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-2003
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ABX76579
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Gaps .. 0

50.0%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 47; ive 0; Mismatches 0; Indels

TGGCACGCAC 20

(first entry)

Homo sapiens WO9620279-A1

LDL; ss.

04-JUL-1996

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95WO-US016000.

11-DEC-1995;

WO9620279-A1 04-JUL-1996.

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The invention relates to a peptide nucleic acid capable of hybridising to a target sequence of Mycobacterial rDNA, precursor rRNA or rRNA (5s, 16s or 1235) forming detectable hybrids. Also included are detecting a target sequence of mycobacteria in a sample comprising contacting rRNA or rDNA in the sample with peptide nucleic acid probes (hybridisation takes place between the probe and the rRNA or rDNA, observing or measuring any formed detectable hybrids and ranks, observing or measurement to the presence of a target sequence of mycobacteria in the sample, and a target sequence of mycobacteria in particular a target sequence of mycobacterial in particular and target sequence of mycobacterial in particular and target sequence of mycobacterial and target sequence of mycobacterial and water present in a sample, e.g. sputum, laryngeal swabs, gastric lavage, bronchial washings, biopsies, aspirates, expectorates, body fluids, urine, tissue sections as well as food samples, soil, air and water or mycobacteria. It is able to hybridise to Mycobacterial precursor the mycobacteria. It is able to hybridise to Mycobacterial precursor therefore avoiding a risk of interfering with the morphology of the cells. TRNA around position 473-477, associated with 165-mediated streptomycin residence.
                                                                                                                                                                                                                                                                                                               Peptide nucleic acid probes for detecting target sequences of Mycobacteria in samples, e.g., sputum, which are capable of hybridizing to a traget sequence of mycobacterial rDNA, precursor rRNA or rRNA forming detectable hybrids.
                                                                                                                                                                                                                  Stender H, Lund K, Mollerup TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 40; 74pp; English.
                         07-APR-2000; 2000US-00544934.
                                                                       07-APR-2000; 2000US-00544934.
                                                                                                                                                                 (MOLL/) MOLLERUP T A.
                                                                                                                                                                                                                                                                   WPI; 2003-174116/17
                                                                                                                      STENDER H.
                                                                                                                      (STEN/)
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Score 10; DB 1; Length 15; Pred. No. 55; 0; Indels 0; Indels Sequence 15 BP; 1 A; 6 C; 6 G; 2 T; 0 U; 0 Other; 50.0%; 100.0%; Query Match Best Local Similarity 100. Matches 10; Conservative

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Gaps ö

> 8 CGCTGGCACG 17 CGCTGGCACG 14 셤

AAT49650 standard; RNA; 15 BP 28-FEB-1997 (first entry) AAT49650;

Human CETP HH ribozyme target sequence #286.

Hammerhead ribozyme, cholesterol ester transfer protein, mRNA cleavage, neutral lipid transfer; plasma lipoprotein, atherosclerosis, atherectomy; reverse cholesterol transport; high density lipoprotein, therapy, CETP, familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia; peripheral vascular disease; hyperberalipoproteinaemia; angloplastic restenosis; low density lipoprotein; diabetes; HDL; human;

NT-3; neurotrophin 3; active; refolded; differentiation; research; human; expression; protein induction; enzyme expression; primer; PCR; ss.

JP09121886-A

Synthetic.

Primer NGFTE-4 used to construct vector to express neurotrophin-3

(first entry)

15-SEP-1997

Homo sapiens

AAT49608-T49863 represent target sequences for the human cholesterol
ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881CET 510137). CETP is a 74 kD glycoprotein that facilitates neutral lipids
transfer between plasma lipoproteins. The numbering of the targets refers
transfer between plasma lipoproteins. The numbering of the targets refers
to the position of the cleavage site in full length CETP. The ribozyme
condition of the cleavage site in full length CETP. The ribozyme
is immediately upstream. The ribozymes are able to cleave mRNA from the
can be inhibited CETP, thereby blocking synthesis and/or expression of the
mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
can be inhibited (or eliminated) thereby preventing the reduction in size
density of the high density lipoproteins (HDL), prolonging HDL half life,
and therefore increasing HDL levels. The ribozymes can be used to treat
conditions associated with abnormal levels of cETP, specifically familial
conditions associated with abnormal levels of GETP, specifically familial
conditions associated with abnormal levels of HDL and low
ascular complications of diabotes, transplant, atherectony and
cangioplastic restences; by inhibiting CETP, the levels of HDL and low
density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
(a decrease in LDL levels, and a corresponding increase in HDL levels).
The HH ribozymes can also be used diagnostically to study genetic drift
cand mutations in diseased cells, and to detect CETP gene, they have low non-New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia. . 0 49.0%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 61; 2; Indels Mcswiggen J, Bisgaier C, Sequence 15 BP; 2 A; 7 C; 4 G; 0 T; 2 U; 0 Other; 0; Mismatches Claim 4; Page 30; 72pp; English. AAT70096 standard; DNA; 15 BP. (RIBO-) RIBOZYME PHARM INC (WARN) WARNER LAMBERT CO. Stinchcomb D, Query Match
Best Local Similarity 84.6
Matches 11; Conservative 6 CICGCIGGCACGC 18 15 creecreeaages 3 WPI; 1996-321852/32. specific activity Couture L, AAT70096; AAT70096 à BXSXXXXXXXXXXXXXXX

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AAX75739;
                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                    AAT70094-96 are primers used to construct a vector capable of expressing human neurotrophin 3 (NT-3). Active NT-3 is produced by the method of the invention, which comprises transforming a prokaryotic host cell with an NT-3 gene to express the NT-3, and then NT-3 produced is refolded correctly in a redox buffer. The active NT-3 produced by the method can be used as a reagent for research on the differentiation of cells,
                                                                                                                             Preparation of active correctly folded neurotrophin-3 - which can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT80036-T80041 represent amplification primers for the alpha2 integrin coding sequence. The primers represented in AAT80030-T80035 are used for
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of nephropathy in mammals - by comparing integrin subunit expression in a tissue sample compared to a control tissue sample.
                                                                                                                                                                                                                                                           genetic expression and induction of protein and enzyme expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR; polymerase chain reaction; primer; amplify; alphal integrin; alpha2 integrin; glomerulopathy; diabetes; nephropathy; ss.
                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                    Score 9.8; DB 1; Length 15;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                        cell differentiation, and protein expression research
                                                                                                                                                                                                                                                                                 Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mauer
                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                Disclosure; Page 7; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 35; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0001387P.
95US-0001861P.
96US-0016700P.
                                 96JP-00220963
                                                         95JP-00217032
                                                                                                                                                                                                                                                                                                       49.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT80039 standard; cDNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                     7 TCGCTGGCACGCA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha2 integrin primer #4
                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                              (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                                                                                                                                                                                                                            TCCCTGGCATGCA
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                                                                                                      WPI; 1997-314237/29
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                 22-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1997
                                                         25-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9704133-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1996;
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03-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT80039;
                                                                                                                                                                                                                                                                                                         Query Match
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the amplification of the alphal integrin coding sequence. These sequences can be used in the method of the invention. The method of the invention is for the identification of a mammal having, or at risk of developing, glomerulopathy. The method comprises analysing a tissue sample from a mammal known to contain cells expressing integrin RNA or protein for integrin subunit expression. The integrin subunit expression in the sample is then compared with a control tissue sample, where altered can be modified to identify a mammal with diabetes who has, or is at risk of developing, secondary pathological changes associated with diabetes. An increase in alpha2,3,5 or beta-1 integrin expression and/or a decrease in alpha1 expression is diagnostic of increased risk of nephropathy. The methods can be used to determine if patients are likely to develop severe nephropathy and to monitor progress of disease during treatment protocols
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fine like tyrosine kinase 1 (fit-1), kinase insert domain containing receptor (KDR) and/or feetal liver kinase 1 (fik-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human flt-1 and KDR hammerhead ribozyme target site #73
                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                                                                                                                                                                      49.0%; Score 9.8; DE 84.6%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 192; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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96US-00584040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX75739 Standard; RNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGACTCGCTGG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Argracrcacres 15
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 84.6
les 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-259017/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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11-JAN-1996;
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AAF45958 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New haplotypes of the FKS06-binding protein 8 gene, useful for genotyping that gene in individual and to design new therapy for associated disease such as immunosuppression and cancer.
vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FX506-binding protein 8; FXBP8; haplotyping; polymorphism; cancer; ss; immunosuppression; human; allele-specific oligonucleotide; ASO; probe.
                                                                                                                                                                                        Gaps
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                                                                                                                                 49.0%; Score 9.8; DB 1; Length 15; larity 61.5%; Pred. No. 61; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human FKBP8 allele-specific oligonucleotide (ASO) probe.
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                                                                                             Seguence 15 BP; 3 A; 2 C; 5 G; 0 T; 5 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 13; 98pp; English.
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AUGGAAUCUCUGG 13
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                                                                                                                                                                Local Similarity
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Stephens JC;
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Matches
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                                                                                           cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia, scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense Oligonucleotide, (for Insuln-like Growth Factor [IGF] receptor, IGF binding protein [IGFBP] 2 or IGFBP3), which is capable inhibiting or reducing growth factor mediated cell proliferation, inhibiting or reducing growth factor mediated cell proliferation, inhibiting or reducing growth factor mediated cell proliferation, oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF4151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, build in seful for ameliorating the effects of psoriasis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                    antiproliferative; antiinflammatory; antipsoriatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 39; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MURD-) MURDOCH CHILDRENS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vessels or any other hyperplasia
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IGFBP2 oligonucleotide #797.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wraight CJ, Werther GA,
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                                                                        Antisense therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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Best Local
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AC AAF4
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4 GACTCGCTGGCACGC 18

GACACCCYGGCACCC 1

RESULT 33

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cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; shin discorder; Insulan-like Growth Factor I receptor; IGF1.1; pityriasis; IGF binding procein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrheea; ruba; keatoosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 screeptor, IGF binding protein [IGFBP]-2 or IGFBP], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, incoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovosscular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to a method for ameliorating the effects of
                                                                                                antiproliferative; antiinflammatory; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.0%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MURD-) MURDOCH CHILDRENS RES INST.
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                 30-MAR-2001 (first entry)
                                                          IGFBP2 oligonucleotide #79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wraight CJ, Werther GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-041421/05
                                                                                              Antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                        WO200078341-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation.
                                                                                                                                                                                                                                                                                   Homo sapiens.
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AAF45957
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AC AAF45
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DT 30-MA
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DE IGFBP
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Edmondson SR;

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisone oligonicleotide, (for Insulin-like Growth Pactor [IGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBB], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonicleotide which can be used to design the antisense oligonicleotide which can be used to design the antisense oligonicleotides of the present invention (see AAF41515 and AAF45153 or A5161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pliaris, serborrhoea, keloids, keratosis, chthyosis, scleroderma, warts, benign growths, cancers of the skin, a hopparance of the sin, and paran or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ameliorating the effects of a disorder, e.g. psoriasis, by administering V (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin disorder, Insulin-like Growth Factor 1 receptor, IGF-1, pityriasis,
          Antisense therapy, antiproliferative, antinflammatory, antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatoolsis, neoplasia; solaroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 4 A; 6 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                        (MURD-) MURDOCH CHILDRENS RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CJ, Werther GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACTCCCTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-041421/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                          WO200078341-A1.
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                 21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001
                                                                                                                                                                                                                                                                                 28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF45236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wraight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF45236
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Gaps .,

2; Indels

0; Mismatches

BP.

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IGF binding protein, IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; Keartosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasis kidney disease; neovascular condition of the retina; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for ameliorating the effects of akin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBB]-2 or IGFBB), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4151 and AAF45151-745161). The method is useful for ameliorating the effects of psoriasis, nebhods is pityriasis, ruba, plaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition growth factor-mediated malignancies, other sclerotic disease, hidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                    Wraight CJ, Werther GA, Edmondson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 34; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                        (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vessels or any other hyperplasia
                                                                                                                                                                                                                                                                   21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-041421/05.
                                                                                                                                                                              WO200078341-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation.
                                                                                                                                                                                                                                                                                                                21-JUN-1999;
                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                        28-DEC-2000
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99US-0140345P

Sequence 15 BP; 0 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

49.0%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 61; arive 0; Mismatches 2; Indels 6 CTCGCTGGCACGC 18 crederederede 15 11; Conservative Query Match Best Local Similarity ద Š

. 0

0; Gaps

AAF45242 standard; DNA; 15 IGFBP2 oligonucleotide #81 30-MAR-2001 (first entry)

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell Proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease;

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an anticompleted decide, (for Insulin-like Growth Pactor [GGP]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the artisense oligonucleotide which can invention (see AAF45151 and AAF45153-F4516). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition of the retina, the print factor mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or Gaps 49.0%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 61; tive 0; Mismatches 2; Indels Seguence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other; Wraight CJ, Werther GA, Edmondson SR; retina; (MURD-) MURDOCH CHILDRENS RES INST. Example 6; Page 34; 201pp; English. the 21-JUN-2000; 2000WO-AU000693. 99US-0140345P. Query Match
Best Local Similarity 84.6
Matches 11; Conservative ŏţ neovascular condition WPI; 2001-041421/05. WO200078341-A1 inflammation. Homo sapiens. 21-JUN-1999;

ö AAF45237 standard; DNA; 15 BP. 6 CTCGCTGGCACGC 18 1 crcecrececes 13 AAF45237; RESULT 38 AAF45237 ò 셤

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IGFBP2 oligonucleotide #76. (first entry) 30-MAR-2001

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; Insulin-like Growth Factor I receptor; IGFP: pityriasis; IGF binding protein; IGFBP-2; IGFBP2; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keardosis; neoplasia; selaroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

Homo sapiens

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antibodisonclebride, (for Insulin-1ike Growth Factor [IGP]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, of indiamation and/or other disorders. The present sequence is an inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAF45153 thy parmeters of the present invention (see AAF45151 and AAF45153 thy prince of the present invention (see AAF45151 and AAF45153 thy present solution such as a neovascular condition such as a neovascular condition of the retina, by prernecese, kidney disease, hyperproliferation of the inside of blood the sesels or any other hyperplasia
                                                                                                                                                                                                                                                                                           Ameliorating the effects of a disorder, e.g. psoriasis, by administering V (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 0 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                         Wraight CJ, Werther GA, Edmondson SR;
                                                                                                                                                                (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 34; 201pp; English
                                                                                 21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                WPI; 2001-041421/05
WO200078341-A1
                                        28-DEC-2000
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DB 1; Length 15; 2; Indels Score 9.8; DB Pred. No. 61; 0; Mismatches Query Match Best Local Similarity 84.6%; Matches 11; Conservative CICGCIGGCACGC 18 ø 8

AAF45241 standard; DNA; 15 BP CICGCICGCICGC 14 g

GFBP2 oligonucleotide #80. (first entry) 30-MAR-2001 AAF45241;

Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin discorder, Insulin-like Growth Factor I receptor, IGF-1; pityriasis; IGF binding proctein, IGFBP-2; IGFBP3; inflammation, psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplamia; kidney disease; neoblation of the retina; ss.

Homo sapiens

WO200078341-A1

28-DEC-2000

99US-0140345P 21-JUN-1999; (MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; CJ, Werther GA, Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF] receptor, IGF binding protein [IGFB] -2 or IGFB3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the effects of psoriasis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, soleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignanoise, other solerotic disease, kidney disease, hyperproliferation of the inside of blood

Gaps .; 0 Similarity 84.6%; Score 9.8; DB 1; Length 15; Similarity 84.6%; Pred. No. 61; Conservative 0; Mismatches 2; Indels / Mac. Local Sim. 11; C Query Match Matches

· 0

CTCGCTGGCACGC 18 CTCGCTCGCCCGC 14

g

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Gaps . 0

BP AAF45956 standard; DNA; 15

(first entry) 30-MAR-2001

IGFBP2 oligonucleotide #795.

WO200078341-A1.

21-JUN-2000; 2000WO-AU000693

99US-0140345P 21-JUN-1999;

21-JUN-2000; 2000WO-AU000693

WPI; 2001-041421/05

Example 6; Page 34; 201pp; English

vessels or any other hyperplasia

Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

9

AAF45956

AAF45956;

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin discorder; Insulin-like Growth Factor 1 receptor; 16F1; pityriasis; IGF binding protein; 1GFBP-2; 1GFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; sclaroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neoblasic of the retina; ss.

Homo sapiens

Example 6; Page 42; 137pp; Japanese.

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonacleoride, (for Insulin-like Growth Factor [GRP] - receptor, IGF binding protein [GRPP] - 2 or IGFBP], which is capable of inhibiting or reducing growth factor mediated cell proliferation, influence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153 - F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pliaris, serborrhoea, keloids, keratosis, chthyosis, scleroderma, warts, benign growths, cancers of the skin, a hypermediated malignancies, other sclerotic brain or skin, growth factor-mediated malignancies, other sclerotic condition of the retina, capable of blood capable of the inside of blood
                                                                                                                                                                                                           Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 15 BP; 3 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 39; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vessels or any other hyperplasia
Werther GA,
                                                                                                        WPI; 2001-041421/05
                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
5
Wraight
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Gaps
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       49.0%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 61; 2; Indels tive 0; Mismatches 2; Indels
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ABL95817 standard; DNA; 15 ABL95817;

BP.

(first entry) 19-JUN-2002 Myeloid progenitor inhibitory factor-1delta23 oligonucleotide #31

Recombinant protein production; drug; reagent; food stuff; ss

Unidentified.

WO200208417-A1

31-JAN-2002

25-JUL-2000; 2000JP-00229064

25-JUL-2001; 2001WO-JP006392

(TAKE) TAKEDA CHEM IND LID

Ito T, Tanaka Y, Kondo M;

WPI; 2002-179906/23

Production of recombinant proteins in prokaryotes or eukaryotes particularly with target proteins obtainable through gene recombination technique, to use as drugs, reagents, raw materials for industries and feeding stuffs.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, PCR, primer; ss, gene therapy, N-acetylgalactosaminidase alpha,
chromosome 22q13.2-q13.31, lysosomal glycohydrolase, screening, SNP;
NAGA-related disease, single nucleotide polymorphism, haplotyping; NAGA;
                              The present invention relates to a method for producing recombinant proteins. The method comprises preparing a recombinant vector for transforming a host cell before culturing the obtained transformant, assaying expression of the reporter gene and confirming high expression of the recombinant proteins are useful as drugs, raw materials for industries and feeding stuffs. Also, the proteins are obtainable on large-scale production. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human N-acetylgalactosaminidase (NAGA) alpha gene ASO primer 2.
                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                DB 1, Length 15;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                    Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                              49.0%; Score 9.8; Di
84.6%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                        ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310/c
ABT05310 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       7 TCGCTGGCACGCA 19
                                                                                                                                                                                                                                                                                                                                                                                                              3 recerrecaced 15
                                                                                                                                                                                                                                                                                                     Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABT05310;
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 42
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The invention comprises the amino acid and coding sequence of the human N-acetylgalactosaminidase (NAGA) alpha protein. The invention specifically comprises novel polymorphic aites identified within the NAGA gene. The NAGA gene is located on chromosome 22q13.2-q13.31, and encodes a lysosomal glycohydrolase that cleaves alpha-N-acetylgalactosaminyl moieties in glycoconjugates. The NAGA DNA and protein sequences of the invention are useful for studying the expression and function of NAGA and for screening candidate drugs to treat diseases related to NAGA activity. The NAGA gene polymorphisms identified in the present invention are useful for haplotyping and genotyping the NAGA gene of an individual. The present DNA sequence represents an N-acetylgalactosaminidase gene allelespecific oligonucleotide primer New genetic variants of isolated N-acetylgalactosaminidase (NAGA), gene, useful for therapeutic purposes, for studying the expression function of the polynucleotide, and for expressing NAGA protein. Claim 16; Page 13; 91pp; English. ABT05310/C
XX
ACCOMP
AC

Parks KE

Koshy B,

Kazemi A,

Duda A,

WPI; 2002-566449/60.

(GENA-) GENAISSANCE PHARM INC.

07-JUN-2001; 2001WO-US018456. 07-JUN-2000; 2000US-0210110P.

WO200194637-A1. Homo sapiens.

genotyping.

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13-DEC-2001

Sequence 15 BP; 2 A; 3 C; 7 G; 2 T; 0 U; 1 Other;

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Gaps

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Indels

7

1; Length 15;

В

Score 9.8; DB Pred. No. 61; 0; Mismatches

49.0%; 84.6%;

Sequence 15 BP; 1 A; 3 C; 9 G; 0 T; 2 U; 0 Other;

SO

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Gaps

; 0

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Genetic affinity, virus, genetic relative, node, bifurcating tree, 88; genetic relationship, signature probe, phylogenetic affinity, space flight, medicine, indoor air quality, bioweapon, mass destruction, epidemic, phylogenetic tree, air filtrate; government building, bioterrorism agent, molecular beacon, bacteria; Bacillus, Kohne approach.
                                                                                                                                                                                                                                                                                                                                                                                                     Determining the genetic affinity of organisms or viruses useful in bioterrorism, comprises determining which nodes in the bifurcating of genetic relationship that designs the signature probes produces hybridization signal.
           Length 15;
                            Indels
                            2,
            DB 1;
           Score 9.8; DB Pred. No. 61; 0; Mismatches
                                                                                                                                                                        RNA seguence #5, for sample identification.
                                                                                                                                                                                                                                                                                                                                                 Elo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 36; 62pp; English
                                                                                                                                                                                                                                                                                                                                                (TECH-) TECHNOLOGY LICENSING CO
                              ..
0
                                                                                                                                                                                                                                                                                                                                                                 Ζ;
                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                           26-JAN-2002; 2002WO-US002564
                                                                                                                                                                                                                                                                                                                             26-JAN-2001; 2001US-0264403P
           49.0%;
Ouery Match
Best Local Similarity **..
11; Conservative
                                                                                                                 ABS59479 standard; RNA; 15
                                                                                                                                                                                                                                                                                                                                                                   Zhang
                                                                                                                                                      (first entry)
                                                 4 GACTCGCTGGCAC 16
                                                                   13 GCCTCGCTAGCAC 1
                                                                                                                                                                                                                                                                                                                                                                   д,
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-619174/66
                                                                                                                                                                                                                                                                                                                                                                    Wilson
                                                                                                                                                                                                                                                                       WO200259348-A2
                                                                                                                                                      05-NOV-2002
                                                                                                                                                                                                                                                                                         01-AUG-2002
                                                                                                                                     ABS59479
                                                                                                                                                                                                                                                                                                                                                                    GE,
                                                                                              RESULT 43
ABS59479/
                                                                                                                                                                                                                                                                                                                                                                     Fox
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The present invention relates to a new method for determining the genetic affinity of organisms or viruses in the test sample. The method involves confernitying the closest known genetic relatives of the organisms or virus confernitying the closest known genetic relations of genetic by determining which nodes in the bifurcating tree of genetic consetul in identifying the phylogenetic affinity of an unknown organism cuseful in identifying the phylogenetic affinity of an unknown organism cuseful for unanticipated problems involving microorganisms that concerns space flight, medicine, indoor air quality, bloweapons of mass consequences are useful in the chybridisation to determine the phylogenetic tree positions of the chybridisation to determine the phylogenetic tree positions of the chybridisation to determine the phylogenetic tree positions of the chybridisation to determine the phylogenetic tree positions of the chybridisation to determine the phylogenetic tree positions of the nected as soluted. TRNA was enriched using DNAse and RNA fragmented by heating. Probes specific to several known bioterrorism agains of negative results. Molecular beacon based scoring of signature sequences reveals the presence of unexpectedly high concentrations of bacteria with genetic affinity to genes and selfinity of organisms in the test sample. The methodology is more general than the specifically targeted tests of the Kohne approach, and faster and more convenient than detailed sequence sequences of the rNAMs or their encoding DNA. The present nucleic acid sequence represents an RNA sequence that was used in the methods of the invention for sample identification
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DB 1; Length 15;

Score 9.8;

49.08;

Query Match

Sequence 15 BP; 1 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

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The sequences given in ABQ80141-52 represent primers which were used to identify wild type and variant loci in the human interleukin 4 receptor identify wild type and variant loci in the human interleukin 4 receptor (IL4R). These primer sequences were used in the method of the invention of comprises detecting the presence of an insulin dependent diabetes mellitus (IDDM) -associated interleukin 4 receptor allele in a nucleic or display ample of the individual, where the presence of the allele in a nucleic the individual where the presence of the allele in a nucleic the single nucleotide polymorphism (SNP) within the IL4R gene listed in the individual's risk for type 1 diabetes. The method identifies one or not single nucleotide polymorphism (SNP) within the IL4R gene listed in individual's risk for type 1 diabetes. The IL4R SNP's are also useful for determining an individual's risk for any autoimmune disease or condition or any T helphet type 1 mediated disease, e.g. rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease, systemic lupus erythematosus, psoriasis, scleroderma, Grave's disease, systemic individual's risk in scleroderma, Grave's disease, or Hashimoto's contraction or Hashimoto's contraction or Hashimoto's contraction or many many many many sclerolesma, Grave's disease, or Hashimoto's contractions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining an individual's risk for type 1 diabetes, comprises detecting
the presence of an insulin dependent diabetes mellitus-associated
interleukin 4 receptor allele in a nucleic acid sample of the individual.
                                                                                                                                                                                                                                                                                                                                                                                                        Human; interleukin 4 receptor; IL4R; type 1; diabetes; allele; insulin dependent diabetes mellitus; IDDM; myasthenia gravis; PCR; single nucleotide polymorphism; SNP; autoimmune disease; amplify; Thelper type 1 mediated disease; rheumatoid arthritis; primer; multiple sclerosis; inflammatory bowel disease; systemic sclerosis; systemic lupus erythematosus; psoriaais; scleroderma; Grave's disease; Guillain-Barre syndrome; Hashimoto's thyroiditis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Æ,
                                                                                                                                                                                                                                                                                                                                                                    Left primer DBM0112B amplifies IL4R amplicon of 177 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Valdez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noble JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) ROCHE DIAGNOSTICS GMBH. (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bugawan TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 35; 79pp; English.
                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                               ABQ80146 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                 (first entry)
Ouery Match
Best Local Similarity 84.0
                                                                                                   CTCGCTGGCACGC 18
                                                                                                                                             14 cacecroecacec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-248086/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mirel DB,
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                                                                                                                                                                                                                                     Hofmann
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ID AAV32268 standard; DNA; 12 BP.
                                                                                                                                                                  20-DEC-2001; 2001WO-EP015179.
                                                                                                                                                                                        03-JAN-2001; 2001DE-01000127
          21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CTGGCACGCAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 CAGGCACGCAC 1
                                                                                                                                                                                                                                     Conradt
                                 Human skin EST 1769.
                                                                                                                                                                                                                                                          WPI; 2002-590638/63.
                                                                                                                                                                                                               (HENK ) HENKEL KGAA
                                                                                                                                                                                                                                                                                                         e.g. skin cancer.
                                                                                                                      WO200253774-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Random primed
                                                                                                                                                                                                                                    Petersohn D,
                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9813521-A1
                                                                                                                                             11-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining nomeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                   Human, skin, dermatological, vulnerary, antipsoriatic; antiseborrhaeic,
immunosuppressive, antiinflammatory; cytostatic; SAGE, neurodermatitis;
psoriasis, dermatitis, skin cancer; EST, expressed sequence tag; ss.
           Gaps
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           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
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 Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                    Hofmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 24; Page 296; 1345pp; German.
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                                                                                                              BP.
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                                                                                                                                                                                                                                                                                                                  20-DEC-2001; 2001WO-EP015179
                                                                                                                                                                                                                                                                                                                                        03-JAN-2001; 2001DE-01000127
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                           ABV71404 standard; cDNA; 11
                                                                                                                                                        (first entry)
                                 GGACTCGCTGGCA 15
                                                       GGCCTCCCTGGCA 15
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Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    Conradt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGCACGCAC
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-590638/63
                                                                                                                                                                              Human skin EST 9190
                                                                                                                                                                                                                                                                                                                                                             (HENK ) HENKEL KGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. skin cancer.
                                                                                                                                                                                                                                                                       WO200253774-A2.
                                                                                                                                                                                                                                                                                                                                                                                    Petersohn D,
                                                                                                                                                         21-0CT-2002
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                           11-JUL-2002
                                                                                                                                  ABV71404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
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                                                                                              RESULT 46
ABV63983/c
ID ABV639
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AC ABV639
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriais; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; ichthyosis; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting; differential gene expression; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 60;

Matches 10; Conservative 0; Mismatches 1; Indels
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The invention provides a method for the differential screening of gene expression by random primed reverse transcription PCR (RT-PCR). The primer sequences are generated by stimulating PCR reactions on norredundant mammalian nuclectide sequence databank entries containing at least 1,000 bp of coding region. The primers selected, such as the present one, had to meet various criteria such as having an efficiency index between 2-10, having a selectivity index higher than 1, being 12 pp long i.e. 8 C or G and 4 T or A, and each primer differed from the others in at least 5 of the 8 bases at the 3'-and. The invention claims the selected primers make it possible to use internally primed, PCR-based RNA differential gene expression as an advantageous alternative to differential display. The method can also be useful for isolating new coding sequences and to compare known and new genes
                                                                                                                                                                           Differential screening of gene expression by reverse transcription polymerase chain reaction - uses random priming with primers selected for high efficiency and selectivity by computer screening of database(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide SEQ ID NO 22817 for detecting SNP TSC0004487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.0%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 64; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 3 A; 5 C; 2 G; 1 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                  Claim 9; Page 24; 37pp; English
                                                                                (SANR-) FOND CENT SAN RAFFAELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-2000; 2000DE-01019173
                97WO-EP005290
                                                96GB-00020216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABC22800 standard; DNA; 13
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es 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGACTCGCTGG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 GGACTCGTTGG 1
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                                                                                                                  Consalez G, Fesce R;
                                                                                                                                              WPI; 1998-230725/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-657177/75
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              26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                27-SEP-1996;
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Matches
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                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) cligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The cligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The cligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
 typing, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oec or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide SEQ ID NO 22818 for detecting SNP TSC0004487.
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                                                                                                                                                                                                                                                                                                                                                                                Score 9.4; DB 1; Length 13; Pred. No. 68; 2; Indels 1; Mismatches 2; Indels
                                                                        Claim 1; SEQ ID NO 22817; 29pp + Sequence Listing; German
oligonucleotides, useful for diagnosis and cell ed to detect single-nucleotide polymorphisms and
                                                                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                       47.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GACTCGCTGGCAC 16
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 76.9
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 RACTCGCTAACAC 1
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                                           methylation status.
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RESULT 51 ABV99924/c ID ABV99924 standard; DNA; 14 BP.

Viral detection; blood sample; Hepatitis C virus;

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Gaps

Oligonucleotide SU1

24-FEB-2003

ABV99924;

13-JUL-2000; 2000RU-00118422 13-JUL-2000; 2000RU-00118422

RU2186388-C2 Unidentified

27-JUL-2002

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This invention describes a novel method for generating an antisense library targeted to a selected RNA transcript. The methods can be used for identifying target sites for antisense agents and for identifying target sites for antisense-mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, ance only very small libraries need be prepared and assayed. AAZ22783-Z23798 represent RNA fragments derived from the Herpes simplex virus genome which are used to illustrate the method of the invention
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIFO at the print electronic format from WIFO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of antisense libraries, used for identifying antisense agents and for identifying target sites for antisense-mediated inhibition of a
                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; DNA library; identification; multiple cloning site; MCS; inhibition; ss.
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                                                                                                                              47.0%; Score 9.4; DB 1; Length 13; ilarity 76.9%; Pred. No. 68; Conservative 1; Mismatches 2; Indels
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                                                                                                  Sequence 13 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus unknown type
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                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                              AAZ23798 standard; RNA; 14
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                 4 GACTCGCTGGCAC 16
                                                                                                                                                                                                                                 RACTCGCTAACAC 13
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                                                                                                                  Query Match
Best Local Similarity
Thes 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                              ISV RNA fragment 16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selected gene.
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06-NOV-1998;
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                                                                                                                                                                                                                                                                                 RESULT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide nucleic acid, PNA, nucleic acid zygosity, genetic analysis;
scientific investigation, pharmacogenomic, pharmacogenetic, epigenomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                     Method for quantitative detection of hepatitis c virus rna in blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.0%; Score 9.2; DB 1; Length 14; 78.6%; Pred. No. 80; ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 BP; 1 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                         (AMHA=) A MED HAEMATOLOGY RES CENTRE (SUDA/) SUDARIKOV A B.
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 3; 5pp; Russian.
                                                                                                                                                                                                                                                                                                                   Glinshchikova OA, Sudarikov AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD48184 standard; DNA; 14 BP.
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Best Local Similarity 78.6
Matches 11; Conservative
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2; Mismatches

Best Local Similarity 72.7 Matches 8; Conservative

Query Match

GGAUUCGCUGG 13

3 GGACTCGCTGG 13

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47.0%; Score 9.4; DB 1; Length 14; 72.7%; Pred. No. 72;

Peptide nucleic acid; PNA; nucleic acid zygosity; genetic analysis; scientific investigation; pharmacogenomic; pharmacogenetic; epigenomic;

Location/Qualifiers

Unidentified

probe; 88.

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Flu-3 PNA probe used for evaluation of combination oligomers.

(first entry)

24-FEB-2003

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AAD48185;

BP.

AAD48185 standard;

RESULT 53 AAD48185/c

14 CACGCTGACACGTA 1

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The present invention relates to combination oligomers, including block synthesis of combination of oligomers in the absence of a template. The invention relates to a composition comprising a polymucleobase strand and a combination oligomer comprising first and second oligomer blocks that are each independently a peptide nucleic acid (PNA) covalently linked to each other by a linker of at least three atoms in length, where the oligomer blocks are sequences specifically hybridised to a target sequence of contiguous nucleobases in the polymucleobase strand, to form a double stranded target sequence-oligomer complex. The composition is cused for determining a target sequence of contiguous nucleobases and for determining the zygosity of a nucleic acid for a single nucleotide of polymorphism (SNP). The methods are useful in scientific investigation, complexing the zygosity of a nucleic acid for a single nucleotide of polymorphism (SNP). The methods are useful in scientific investigation, contrasts and pathogens in food, beverages, water, pharmaceutical products, viruses and pathogens in food, beverages, water, pharmaceutical products, contiguent, animal, human or environmental origin. They are also useful for the analysis of raw materials, equipment, products or processes used to manufacture or store food, beverages, water, pharmaceutical products, contiguous and materials are useful in areas such as expression analysis, such analysis, genetic analysis of humans, animals, fungi, yeast viruses contiguence is a PNA probe used for evaluation of combination oligomers. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition for determining target sequence of contiguous nucleobases, comprises polynucleobase strand and combination oligomer comprising first and second oligomer blocks that are covalently linked to each other.
                                                                  /note= "This sequence is a peptide nucleic acid i.e. it contains a polyamide backbone instead of a deoxyribose-phosphate backbone"
                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "This base is linked to EE-NH2 group where
represents a linker"
                                                                                                                                                                                                 /note= "This base is linked to F-OEE where F, O represent 5-(6)-carboxyfluorescein, 8-amino-3,6-dioxaoctanoic acid and linker respectively"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fiandaca MJ, Kristjanson MD, Hyldig-Nielsen JJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 64; 149pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                   /*tag= c
/mod base= OTHER
                                                                                                                                                              /*tag= b
/mod_base= OTHER
                                                         base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-2002; 2002WO-US007050.
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  Key
modified_base
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The present invention relates to combination oligomers, including block synthesis of combination of oligomers in the absence of a template. The invention relates to a composition comprising a polynucleobase strand and a combination oligomer comprising first and second oligomer blocks that are each independently a peptide nucleic acid (PNA) covalently linked to each other by a linker of at least three atoms in length, where the oligomer blocks are sequences specifically hybridised to a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for determining target sequence of contiguous nucleobases, comprises polynucleobase strand and combination oligomer comprising first and second oligomer blocks that are covalently linked to each other.
                                                                                                                                                                                                 /mod_base= OTHER
/note= "This sequence is a peptide nucleic acid i.e. it
contains a polyamide backbone instead of a deoxyribose-
phosphate backbone"
                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/mod_base= OTHER
/note= "These bases are linked via 8-amino-3,6-
dioxaoctanic acid linker which is represented in the
specification as O"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /mod_base= OTHER
/note= "This base is linked to BE-NH2 group where
represents a linker"
                                                                                                                                                                                                                                                                                    /mode= This base is linked to F-OEE where F, O represent 5-(6)-carboxyfluorescein, 8-amino-3,6-dioxaoctanoic acid and linker respectively"
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Query Match Best Local S

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a double stranded target sequence-oligomer complex. The composition is used for determining a target sequence of contiguous nucleobases and for determining the zygosity of a nucleic acid for a single nucleotide polymorphism (SNP). The methods are useful in scientific investigation, e.g., for detection, identification and/or enumeration of bacteria, viruses and pathogens in food, beverages, water, pharmaceutical products, personal care products, dairy products, in clinical samples or in samples of pathogens in food, beverages, water, pharmaceutical products, of plant, animal, human or environmental oxigin. They are also useful for the analysis of raw materials, equipment, products or processes used to manufacture or store food, beverages, water, pharmaceutical products, personal care products dairy products or environmental samples. The methods and materials are useful in areas such as expression analysis, SNP analysis, genetic analysis of humans, animals, fungl, yeast viruses and plants, therapy monitoring, pharmacogenetics, pharmacogenetics, epigenomics and high throughput screening operations. The present epigenomics and high throughput screening operations. The present envaluation of combination oligomers. This sequence is a PNA probe used for evaluation of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "This sequence is a peptide nucleic acid i.e. it
contains a polyamide backbone instead of a deoxyribose-
phosphate backbone"
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/note= "This base is linked to EE-NH2 group where
represents a linker"
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                                                                                                                                                                                                                                                                                                                                                                                                      46.0%; Score 9.2; DB 1; Length 14; 78.6%; Pred, No. 80;
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Best Local Similarity 78.6
Matches 11; Conservative
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The present invention relates to combination oligomers, including block sytthesis of combination of oligomers in the absence of a template. The invention relates to a composition comprising a polymucleobase strand and a composition oligomer comprising first and second oligomer blocks that are each independently a peptide nucleic acid (PNA) covalently linked to each other by a linker of at least three atoms in length, where the cligomer blocks are sequences specifically hybridised to a target sequence of contiguous nucleobases in the polymucleobase strand, to form a double stranded target sequence-oligomer complex. The composition is consed for determining a target sequence-oligomer complex. The composition is determining the zygosity of a nucleic acid for a single nucleotide colymorphism (SNP). The methods are useful in scientific investigation, colymorphism (SNP). The methods are useful in scientific investigation, colymorphism (SNP). The methods are useful in scientific investigation, colymorphism in food, beverages, water, pharmaceutical products, viruses and pathogens in food, beverages, water, pharmaceutical products, of plant, animal, human or environmental origin. They are also useful for the analysis of taw materials, equipment, products or processes used to personal care products dairy products or environmental samples. They are also useful for methods and materials are useful in areas such as expression analysis, sentents analysis of humans, animals, fungi, yeast viruses and plants, therapy monitoring, pharmacogenedics, pharmacogenetics, and plants, therapy monitoring, pharmacogenedics, pharmacogenetics, cand plants, therapy monitoring, pharmacogenedics, pharmacogenetics, ceptigenomics and high throughput screening operations. The present complement of sequence is a PNA probe used for evening operation of the invention coligomers.
                                                                                                                                                                                                                                                  Composition for determining target sequence of contiguous nucleobases, comprises polynucleobase strand and combination oligomer comprising first and second oligomer blocks that are covalently linked to each other.
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ID AAZ78944 standard; DNA; 10 BP.
39-MAR-2002; 2002WO-US007050.
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Matches 11; Conservative
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APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells
Co-administration of tumour antigens and
                                                                                                                                                                                                                                                                                                                                                       SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                                                                                                              DB 1; Length 10;
                                                                                     Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   Human dendritic cell SAGE tag, SEQ ID NO:833.
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Local Similarity 100.0%; Pred. No. 69; Pres 9; Conservative 0; Mismatches
 them are used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression) tagg used to identify mRNA transcripts encoding coxpression) tagg used to identify mRNA transcripts encoding coxpression) tagg used to identify mRNA transcripts encoding differentially expressed in monocytes. Preferentially compared differentially expressed in monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while cother transcripts correspond to novel genes. Antigen-presenting cell cativation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytocoxic Tlymphocytes (CTLS). Nucleic can lyse complexication of cytocoxic Tlymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response that can lyse cagainst a tumour antigen; to endulate the genotype of an APC; to screen for agents that modilate expression of differentially expressed genes in a APC; and as hybridisation primers for the dendritic cell differentially expressed genes. Occupancy in a probe and monitoring of diseases related to abnormal capsessed genes, or of their encoded proteins, can be used to identify calls as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 104; 130pp; English.
                                                  98US-0089834P.
98US-0089843P.
98US-008983P.
98US-0089991P.
98US-0089991P.
98US-0089993P.
                                                                                                                                                                98US-0111715P
                            99WO-US013800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts BL, Shankara S;
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ROBERTS B L.
SHANKARA S.
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19-JUN-1998;
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19-JUN-1998;
                           18-JUN-1999;
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19-1107-1998
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Roberts

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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAM63161. Ath64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubsquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 66; 94pp; English.
                                                                                                                                                                                                             Jelculescu VE, Vogelstein B,
                             21-NOV-2000; 2000WO-US031922
                                                                                        99US-00448480
                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS
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Best Local Similarity
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                                                                                    24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                  Expression) tags used to identify mRNA transcripts encoding compression) tags used to identify mRNA transcripts encoding compressed in monocyte-derived dendritic cells compared differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while cher transcripts correspond to novel genes. Antigen-presenting cell corporation of the cytotoxic immune response, particularly against tumour complex, and subsequent recognition by T-cell receptors is alone activate as robust cytotoxic immune response that can lyse complex, and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for cefficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses. Genes tumour antigen; to modulate the genotype of an APC; to screen to capture that modulate expression of differentially expressed genes in the approach of the containing of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify calls as belonging to the monocyte lineage. Cells containing these genes in the are used in active immunotherapy (or to ctimulate production of a colls and promine of antigen-specific effector cells and promine of antigen-specific effector cells and promine of the monocyte or cells and promine of the monocyte or cells and promine or cells and promine and containing the encoded processed genes or of their encoded promine. The containing these genes cells are also become the
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                                                                                                                                                                                   Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
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cancer diagnosis, cell specific gene expression, ss.
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                                                          Shankara
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   (SHAN/) SHANKARA S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polymorphic variants of potassium voltage-gated channel, Shab-
related subfamily, member 1 (KCNB1) gene useful for expressing KCNB1
protein isoform to screen drugs to treat KCNB1 activity-related disease.
                                                           Gaps
                                                                                                                                                                                                                                                                                                            Human; KCNB1; single nucleotide polymorphism; SNP; gene therapy; potassium voltage-gated channel; Shab-related subfamily, member 1; isogene; arrhythmia; seizures; allele-specific oligonucleotide; PCR;
                                                         ;
0
                                                        0; Indels
                         45.0%; Score 9; DB 1; Length 10; illarity 100.0%; Pred. No. 69; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               Human KCNB1 gene primer extension oligo SEQ ID NO: 41.
Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                         primer extension oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 14; 180pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                           AAL45327 standard; DNA; 10 BP.
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Best Loca Matches

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WO200138577-A2 Homo sapiens

31-MAY-2001.

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The present invention provides the protein, gene and cDNA sequences of the human potassium voltage-gated channel. Shab-related subfamily, member 1 (KCNB1) isogene and polymorphisms identified within these sequences. The sequences can be used to screen drugs, which involves contacting the polypeptide with a candidate agent, and to assay for binding activity as a target for drugs to treat arthythma and seizures. The present sequence is a primer extension oligonucleotide described in the invention

Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

DB 1; Length 10; 45.0%; Score 9; DB 1 100.0%; Pred. No. 69; tive 0; Mismatches Local Similarity 100. 4 GACTCGCTG 12 Query Match Best Local S: Matches 9 ò

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GACTCGCTG 2 10 ద

ABL52050 standard; DNA; 10 ABL52050;

BP.

(first entry) 11-JUL-2002 Human SLC18A2 preferred oligonucleotide primer SEQ ID NO:98.

monoamine; Human; solute carrier family 18 member 2; SLC18A2; vesicular movesicular monoamine transporter; VMAT2; polymorphic site; SNP, single nucleotide polymorphism; antiniflammatory; neuroleptic; haplotyping; genotyping; respiratory inflammatory disease; neuropsychiatric disorder; monoaminergic brain system; primer;

Homo sapiens

WO200222652-A2

21-MAR-2002

17-SEP-2001; 2001WO-US042217

15-SEP-2000; 2000US-0232895P

(GENA-) GENAISSANCE PHARM INC.

Sausker Kliem SE, Anastasio AE, Han J,

WPI; 2002-393942/42

Novel genetic variants of soluble carrier family 18 (vesicular monoamine), member 2 gene useful for screening drugs to treat diseases e.g. neuropsychiatric disorders involving monoaminergic brain systems.

Claim 19; Page 15; 183pp; English

The present invention describes an isolated polynucleotide (I) having a sequence (SI) comprising soluble carrier family 18 (vesicular monoamine), member 2 (SLC1822) isogenee selected from 49 isogenees with respices of a sequence (SS) of 40023 bp (see ABL51954), and defined by a corresponding set of polymorphisms whose locations and identities are given in the specification; or a sequence (SS) complementary to (SI). (I) has antithflammatory and neuroleptic activities, and can be used in gene therapy. Methods from the present invention can be used for haplotyping and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known as the vesicular monoamine transporter (WAAT2). (I) is useful in studying the expression and function of SLC18A2, and in expressing the SLC18A2 activity and in studying the effect of the variation on the biological activity of SLC18A2 seel is so the binding affinity of candidate drugs targeting SLC18A2 for the treatment of respiratory RESULT 59
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Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

skin. The present seque (EST) of the invention

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             monoaminergic brain systems. The present sequence represents a preferred oligonucleotide primer for human SLC18A2, which is given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                           Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                              Gaps
neuropsychiatric disorders involving
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llarity 100.0%; Pred. No. 69;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                             ABV63868 standard; cDNA; 11
   Buch
                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                            9 GCTGGCACG 17
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                                                                                                                                                                                                                                                                                                                                                                                             Human skin EST 1654.
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                                                  invention
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ABV71289 standard; cDNA; 11

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(first entry)

21-OCT-2002

ABV71289;

Human skin EST 9075

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; icthhyosis; atopic dermatitis; acne; seborrhas; lupus erythematosus; rosace, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                         In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 103; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                         Conradt M, Hofmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        remplate sequence Seq ID No: 3.
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                                                                                                                                                                                                                         20-DEC-2001; 2001WO-EP015179.
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gene production; primer; 88.
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                                                                                                                                       WO200253774-A2
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                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                            Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Best Local Similarity 100.0%; Pred. No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;
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Claim 24; Page 291; 1345pp; German.

e.g. skin cancer.

ABV65042 standard; cDNA; 11

GGCACGCAC 20

12

ð g 21-OCT-2002 (first entry)

ABV65042;

Human skin EST 2828

Hofmann

Σ

Petersohn D, Conradt

WPI; 2002-590638/63

(HENK) HENKEL KGAA

20-DEC-2001; 2001WO-EP015179 03-JAN-2001; 2001DE-01000127

WO200253774-A2.

Homo sapiens

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(CSIR ) COMMONWEALTH SCI & IND RES ORG.
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les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGACTCG
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02-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                              The invention relates to a method for producing polymucleotides having a defined sequence using rolling templates that successively add nucleotides (ints) to a longer primer strand. The method comprises: (i) incubating, under ammealing conditions, a primer and a template that has a 5'-region not complementary to the primer, a 3'-region complementary to the primer, with the template the ingressor of primer and a non-reactive 3'-reminus, with the template of the ing shorter than the primer; (ii) reacting the primer with at least one in presence of a template-dependent polymucleotide polymerase to at its 3'-end; (iii) separating the template and the extended primer; and (iv) repeating the cycle of (i)-(iii) as often as needed to synthesize the desired polymucleotide. The method is especially used to produce genes or their segments. The method is especially used to produce genes or their segments. The method is especially used to produce synthesis of RNA or DNA and is more efficient than chemical coupling processes. It has higher specificity and eliminates the need for deprotection. The products can be cloned directly. The method avoids problems of waste disposal and includes an inherent editing effect. (failure sequences will not be extended further in subsequent rounds so that purification of the end product is facilitated. Synthesis may take place on a vector, simplifying cloning and sequences with codon usage optimized for a particular host can be prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                               Producing specific polynucleotides using rolling templates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.0%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 79; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                            Disclosure; Page 24; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       remplate sequence Seg ID No: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX34404 standard; DNA; 12 BP
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Best Local Similarity 100...
Aconservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ATGGACTCG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rose FD;
                                                                    WPI; 1999-244045/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HIAT/) HIATT A C. (ROSE/) ROSE F D.
                                         Hiatt AC, Rose FD;
(HIAT/) HIATT A C. (ROSE/) ROSE F D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX34404;
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The invention relates to a method for producing polynucleotides having a defined sequence using rolling templates that successively add nucleotides (IIs) to a longer primer strand. The method comprises: (i) incubating, under annealing conditions, a primer and a template that has a 'region not complementary to the primer, a 3'-region complementary to the 3'-reminus, with the template being shorter than the primer; (ii) reacting the primer with at least one to in presence of a template-dependent polymucleotide polymerase to the in presence of a template-dependent polymucleotide polymerase to the integral of the primer; and (iv) repeating the cycle of (i)-(iii) as often as needed to synthesize the desired polymucleotide. The method is especially used to produce the desired polymucleotide. The method provides fast, accurate, inexpensive synthesis of RNA or DNA and is more efficient than chemical coupling problems of waste disposal and includes an inherent editing effect problems of waste disposal and includes an inherent editing effect problems of waste disposal and includes an inherent editing effect that purification of the end product is facilitated. Synthesis may take place on a vector, simplifying cloning and sequences with codon usage openialized for a particular host can be prepared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth hormone system; Kruppel system; TAT system; OU system; asymmetric hammerhead ribozyme; cleavage; viral infection; bacterial; neoplastic; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
          producing specific polynucleotides using rolling templates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.0%; Score 9; DB 1; Length 12; conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
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/note= "deoxyribonucleotide"
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                                                                    Disclosure; Page 25; 109pp; English.
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ID AAT92438 standard; RNA; 13 BP.
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96US-00627033.
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AAA06013 CAAA06013 STANDARD, 13 BP.
XX
XC AAA06013;
XX
C AAA06013;
XX
C T14-JUN-2000 (first entry)
XX
CFTR gene analysis oligonucleoti
XX
CFTR, cystic fibrosis transmembr
XX
CFTR, cystic fibrosis transmembr
XX
XX
Homo sapiens.
XX
YX
CS-0CT-1995;
YB 22-FEB-2000.
XX
YX
XX
CFCT-1994;
YB 26-OCT-1994;
YB 26-OCT-1995;
YB 26-OCT-1995;
YB 26-OCT-1995;
YB 26-OCT-1995;
YB 26-OCT-1995;
YB 26-OCT-1995;
YB 2
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New asymmetric hammerhead ribozymes have been developed, of the formula:

5'-(N)n'NNN-C-U-G-A-[N-G-A-(N)a-(N)m-P-(N)m-G-A-A-ANDNNNN(N)n-3', where
N = a nuclectide which may be substituted or modified in its sugar, base
or phosphate provided not every N is a ribonuclectide; the hybridising
arms 3'-(N)nNNNNNA and NNN (N)n-5' are each an oligonuclectide (ON)
having a prederamined sequence which is complementary to an RNA target
capture to be cleaved; n and n' = an integer which defines the number of
nuclectides in the ON with the proviso that n =1-5 and n' = 1 to 3; each
solid line represents chemical linkage providing ovorlent bonds between
the nuclectides located on either side; a = an integer which defines a
number of nuclectides with the proviso that a may be 0 or 1 and if 0, the
loop of the compound each m and m' = an integer which is greater than 2;
p = a non-nuclectide linker or a nuclectide linker (N)b, where (N)b
represents an ON which may be present with the proviso that b = an
ribozymes can be used for cleaving RNA target sequences. They can be used
for cleaving diseases (e.g. viral or bacterial infections, neoplastic
conditions, or psoriasis). They can also be used as diagnostics, e.g. to New asymmetric hammerhead ribozymes - used for cleaving target RNA for treating e.g. viral or bacterial infection, neoplastic conditions or Disclosure; Page 34; 49pp; English gene mapping psoriasis

ô 0; Indels 45.0%; Score 9; DB 1; Length 13; 100.0%; Pred. No. 84; 0; Mismatches 0; Indels Sequence 13 BP; 3 A; 5 C; 3 G; 1 T; 1 U; 0 Other; Conservative

TGGACTCGC 10 9 TGGACTCGC 1 N

CFTR gene analysis oligonucleotide probe SEQ ID NO:23.

CFTR; cystic fibrosis transmembrane conductance regulator; detection; mutation; probe; human; hybridisation; ss.

Miyada CG; Chee M, Lobban PE, Hubbell EA, Sheldon EL, Lipshutz RJ, Morris MS, Fodor SPA;

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The present invention describes an array of nucleic acid probes

comprising probes with a segment of at least 6 nuclectides complementary

comprising probes with a segment of at least 6 nuclectides complementary

to the CFTR (cystic fibrosis transmembrane conductance regulator) gene,

where the segment includes at least 1 interrogation position

complementary to a nuclectide in the CFTR gene sequence; and (2) second,

third and fourth probe sets, each comprising probes identical to those in

chird and fourth probe sets, need to moprision is occupied by a different

contlementary to AAAO6391 to present CFTR gene analysis a

cuclectide. AAAO6391 to passent CFTR gene analysis a

controlled probes for use in the exemplification of the present

invention. The present invention also describes a method of comparing a

crarget nucleic acid with a reference sequence consisting of comparing a

crarget nucleic acid with a reference sequence consisting of a

probes inmobilised on a solid support; (b) comparing the relative

crapt moding of two corresponding probes from the first and second

probe sets; (c) assigning a nucleotide in the target sequence as the

complement of the interrogation position of (b) by comparing the relative

craptic binding; and (d) repeating (b) and (c) by comparing the relative

craptic binding; and (d) repeating (b) and (c) by comparing the first and

second probe sets until each nucleotide of interest in the target

sequence has been assigned. The array is useful for analysis of the CFTR

crays and the corresponding of the array is useful for analysis of the CFTR

crays and the corresponding of the cFTR

crays and the cFTR

crays and the cFTR

crays array is useful for analysis of the CFTR

crays and crays are corresponding of the cFTR

crays and crays are correspondent or correspondent or crays of the cFTR

crays and crays are correspondent or correspondent or
                    An array of nucleic acid probes immobilized on a solid support, useful for identifying mutations in the cystic fibrosis transmembrane
                                                                                                                                                                            Disclosure; Col 73; 114pp; English.
                                                                                                        conductance regulator.
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Sequence 13 BP; 0 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Gaps . 0 0; Indels 45.0%; Score 9; DB 1; Length 13; 100.0%; Pred. No. 84; ative 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

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Gaps

AAZ40108 standard; DNA; 13 BP. 18-FEB-2000 (first entry) AAZ40108; RESULT 67 AAZ40108/ XYZXEXEXEXEXEXEXEXEXEXEXEXEX

Detection probe, electronic detection, conductive oligomer, capture probe, nucleic acid detection, genetic diagnostic, viral detection, bacterial detection, gene amplification detection, Detection probe #D203_1.

DNA fingerprinting; ss

Synthetic.

W09957319-A1

11-NOV-1999

98US-0084425P. 98US-0084509P. 99WO-US001703 06-MAY-1998; 06-MAY-1998; 17-AUG-1998; 27-JAN-1999;

(CLIN-) CLINICAL MICRO SENSORS

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Tue Jun

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Blectrode with a monolayer of conductive oligomers and insulators, with attached covalent capture ligand, used for, e.g. clinical or environmental assays.
                                                                                                                                                                                                                                                                                                        Example 8; Page 97; 143pp; English
                                                                                                                                                                                                                                                                               WPI; 2000-052978/04.
                                                                                                                                                                                                                      WO9957317-A1
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17-AUG-1998;
                                                                                                                                                                    24~FEB-2000
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                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                       Bamdad C,
                                                                                                                                                            AAZ40248;
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This sequence represents a detection probe that can be used in the composition of the invention. The composition comprises an electrode with composition of the invention. The composition comprises an electrode with composition of the invention of conductive oligomers (1) and insulators, and a covalently attached capture binding ligand. The composition is cused: (1) for environmental or clinical assays, for practically any analyte for which a ligand is available, e.g. pesticides, therapeutic or illicit drugs, hormones, immunoglobulins, nucleic acids, tumour or other cells, bacteria, viruses, antigens; (2) to screen for potential cells, bacteria, viruses, antigens; (2) to screen for potential composition analysis, e.g. detecting disease-associated genes or mutations; (4) for forensic fingerprinting; and (5) to detect successful amplification in polymerase chain reactions. Electron transfer molecules (ETMs) can be detected directly on the surface of (4) containing (1). (A) shield the electrode from solution components and reduces the degree of sensitivity, e.g. 20-50 per recruitment linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; electron transfer moiety, ETM; detection; amplification;
forensics; diagnosis; quality control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 45.0%; Score 9; DB 1; Length 13; 100.0%; Pred. No. 84; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 BP; 3 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
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|label= OTHER
'note= "ETM attachment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF30135 standard; DNA; 13 BP.
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/label= OTHER
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es 9; Conservative
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                           This sequence represents a detection probe that can be used in the composition of the invention. The compositions comprise: (a) an electrode compositions of the invention. The compositions comprising it is a monalwayer comprising of an electrode comprising; (i) a monalwayer comprising is an electrode capture probe; and either (b) a target sequence comprising a portion that can hybridize to the probe and has at least 1 covalently attached electron transfer moiety (ETM); or (c) a label probe comprising a portion that can hydridise to a component of an assay complex and a second portion to hydridise to an assay complex component and has at least 1 covalently attached ETM. The probes are useful for the detection of a target nucleic acid sequences in complex genetic diagnostics, viral or bacterial detection, forensic 'DNA fingerprinting', and for detecting successful gene amplification in PCR. The ETM's can be used as intermediates in the preparation of metallocene-
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                                            Components for the electronic detection of nucleic acids using conductive oligomers monolayers linked to probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection probe; electronic detection; conductive oligomer; label probe; capture probe; nucleic acid detection; microorganism detection; genetic analysis, disease-associated gene detection; mutation detection; forensic fingerprinting; gene amplification detection; electron transfer molecule; ss.
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Best Local Similarity 100.0%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 13 BP; 3 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                              Example 7; Page 94; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CLIN-) CLINICAL MICRO SENSORS INC.
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98US-0084652P.
98US-00135183.
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    WPI; 2000-038823/03
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The present sequence represents a positive control label probe containing

Example 7; Page 123; 198pp; English.

moiety.

Detection of a target nucleic acid for screening blood, water and food samples comprises using amplification techniques and an electron transfer

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Gaps

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of expression differential.

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lor 2 metal complexes as electron transfer moleties (ETMs). Experiments were performed to compare different ETM attachments. A detection probe complementary to the detection probe) and negative (i.e. probes not complementary to the detection probe) and negative (i.e. probes not complementary to the detection probe) control labels were added. The electrodes were used in AC detection methods. The invention relates to methods useful in the detection of nucleic acids using a variety of amplification techniques, including both signal amplification and target amplification. Detection proceeds through the use of an ETM, preferably a metallocene and especially a ferrocene, that is associated with the nucleic acids, either directly or indirectly, to allow electronic detection of the ETM using an electrode. The extremely sensitive and specific probes can detect target sequences without removal of unhybridised probe, and are useful in a variety of forensic (e.g. DNA fingerprinting), research, clinical (e.g. genetic diagnosis), quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining differential display of gene expression, useful for monitoring drug responses at the gene expression level and locating genes involved in a particular response, by comparisons between mono-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ39834-38 represent target oligonucleotides which were used to test for complementarity binding on three different types of membrane, in the course of the invention. The specification describes a method of determining differential display of gene expression, by comparison of mono-length cRNA libraries. These libraries are probe hybridised to accessible ordered arrays to determine differential hybridisation display sites between mono-length segment libraries and to locate genes of expression differential. The methods are useful for determining differential hybridisation display sites between mono-length segment
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                                                                                                                                           45.0%; Score 9; DB 1
100.0%; Pred. No. 84;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 43; 73pp; English.
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Best Local Similarity
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GRNA libraries.
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AAZ99838
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complementarity binding on three different types of membrane, in the complementarity binding on three different types of membrane, in the course of the invention. The specification describes a method of determining differential display of gene expression, by comparison of mono-length cRNA libraries. These libraries are probe hybridised to accessible ordered arrays to determine differential hybridisation display segment libraries and to locate genes of expression differential. The methods are useful for determining ciferential hybridisation display sites between mono-length segment libraries and to locate genes of expression differential. The methods are useful in gene identification related to complex traits. The methods also useful in gene identification related to complex traits. The methods also bermit monitoring drug responses at the gene expression level and cotating genes involved in a particular response. The methods are also useful for pharmacogenomic research in evaluating how variability in genetic background influences positive or negative response to a drug
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libraries and to locate genes of expression differential. The methods are also useful in gene identification related to complex traits. The methods also permit monitoring drug responses at the gene expression level and locating genes involved in a particular response. The methods are also useful for pharmacogenomic research in evaluating how variability in genetic background influences positive or negative response to a drug
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                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mono-length cDNA library, differential display, gene expression, gene identification, drug response, probe, ss.
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                                                                                                                                                                 Query Match
Best Local Similarity 83.3%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 2; Indels
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                                                                                                                                  Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of probe oligonucleotide H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 43; 73pp; English
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AAZ99833/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF99999, ABF00010-ABF99999 and ABI00010-ABF99999 as obtained in electronic form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                 SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                      Oligonucleotide primer SEQ ID NO 286569 for detecting SNP TSC0012735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 286569; 29pp + Sequence Listing; German.
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ID ABH86514 standard; DNA; 12 BP.
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                  22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
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les 10; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH00010-ABF99889 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 310621 for detecting SNP TSC0024025.
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                            Gaps
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                          2; Indels
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83.3%; Pred. No. 88;
    Pred. No. 88;
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  83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                       3 GGACTCGCTGGC 14
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Gaps

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2; Indels

ABH86576

RESULT 73 ABH86576 ID ABH86 XX AC ABH86

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designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 286488; 29pp + Sequence Listing;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The coligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 286507; 29pp + Sequence Listing; German.
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44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred, No. 88;
Matches 10; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoshie methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraated genomic DNA. The oligonucleotides are used for disgnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                         / Match Local Similarity 83.3%; Pred. No. 88; DB 1; Length 12; Local Similarity 83.3%; Pred. No. 88; 2; Indels tes 10; Conservative 0; Mismatches 2; Indels
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Set of oligonuclectides, useful for diagnosis and cell typing,

Berlin

Piepenbrock

olek A,

WPI; 2001-657177/75

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Oligonucleotide SEQ ID NO 9569 for detecting SNP TSC0002510.

(first entry)

20-FEB-2002

ABC09578;

BP.

DNA; 13

ABC09578 standard;

RESULT 78

ABC0957

12 GCACGCACGCAC 1

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC099889, ABC00100-ABE99889, ABC0010-ABE99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence are obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 88;
0; Mismatches 2; Indels
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83.3%; Pred. No. 88;
:ive 0; Mismatches
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Best Local Similarity 83.3<sup>3</sup>
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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.larity 83.3%; Pred. No. 93;
Conservative 0; Mismatches 2; Indels
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ABC09579 standard; DNA; 13
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Best Loc 10; Conserva
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecule, Hepatitis C virus, HCV, Hepatitis B virus, HBV, RNA stability, RNA expression, RNA synthesis, antisense; enzymetic nucleic acid, harmerthead ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; anti-HCV; viral replication; degenerative, disease state; HBV infection; HCV infection; cirrhosis; liver failure, hepatocellular carcinoma; hepatotropic; cytostatic; virucide; anti-filmmatory; target; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 9570; 29pp + Sequence Listing; German.
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Matches
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HEV) or Hepatitis B virus (HEV) or an entaymetic acids such as harmerhead ribozymes, DNAzymes, and enzymatic nucleic acids such as harmerhead ribozymes, DNAzymes, CC are nucleic acid decoup molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or infection of HCV. The compounds and methods of the invention and dor nethods of the invention and dor the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a target for one of the anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16S rRNA; probe; detection; procine atrophic rhinitis; hybridisation;
Bordetella bronchiseptica; pig raising; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13 BP; 1 A; 2 C; 6 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcswiggen J, Morrissey D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 318; 387pp; English
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                                                                                                          26-MAR-2001, 2001US-00817879.
08-JUN-2001, 2001US-0087478.
08-JUN-2001, 2001US-0296876P.
24-OCT-2001, 2001US-0337055P.
05-DEC-2001, 2001US-0337055P.
                                                      26-MAR-2002; 2002WO-US009187
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                                                                                                                                                                                                                                                                                                 RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 83.3
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ACTCGCTGGCAC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macejak D,
Roberts E;
                                                                                                                                                                                                                                                                                                                       BLATT L.
MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
PAVCO P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-229207/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROBERTS E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRAPER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
22-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection.
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                                                                                                                                                                                                                                                                                                                              (BLAT/)
(MACE/)
(MCSW/)
(MORR/)
(PAVC/)
(LEEP/)
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(ROBE/)
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ID AAQ6
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SON COURT OF THE STANDARD STAN
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Hepatitis C virus. WO200281494-A1

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                                                                                                                                                                                                                   B.bronchiseptica 16s rRNA fragments - used as probes in the detection of porcine atrophic rhinitis.
                                                                                                                                                                                                                                                                                       (AAQ64009-Q64031) are fragments of the 16S rRNA gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAGE tag, serial analysis of gene expression, antigen-presenting cell, APC, moncoyte-darived dendritic cell, differential gene expression, immunostimulatory cofactor, costimulatory factor, CTL, cytotoxic T-lymphocyte, tumour antigen, immunotherapy, anticancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.0%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human dendritic cell SAGE tag, SEQ ID NO:1384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Mismatches
                                                                                                                                                 (NISE-) NIHON SEIFUN KK.
(ZENK-) ZENKOKU NOGYO KD RENGOKAI
                                                                                                                                                                                                                                                              Claim 1; Page 11; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0089833P.
98US-0089844P.
98US-0089883P.
98US-0089991P.
98US-0089992P.
98US-0089992P.
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                                                                                           92JP-00150688.
                                                                                                                      92JP-00150688
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             Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                          sednences
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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                                      JP05336999-A
                                                                                           10-JUN-1992;
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19-01-NUT-01
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                                                                  21-DEC-1993
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Sequences AAZ7573-Z79709 represent SAGE (Bernal analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimmlatory coffactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while or preferentially or differentially expressed in dendritic cells, while or ther transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell or their transcripts correspond to novel genes. Antigen-presenting cell or their antigen presentation via the MEC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone cells. Thumour antigen presentation via the MEC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone certivation of cytotoxic T-lymphocytes (CTES). Nucleic can lyse the tumour cells, immunostimulatory coffectors also being required for the tumour cells, immunostimulatory coffectors also being required for the tumour antigen; to modulate expression of diseases (corresponse, particularly sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate expression of these genes, or of their encoded proteins, can be used to a prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cells containing them are used in active immunotherapy (or to stimulate production of the progness and monitoring of diseases related to abnormal component or endogenous APCs and upregulates the APCs for the presentation of costimulatory factors ensures adequate antigen factor cells or presentation of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      solated polynucleotides differentially expressed in antigen-presenting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells, useful in gene vaccines against cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 104; 130pp; English.
                                 98US-0090030P
98US-0090033P
98US-0090040P
98US-0090041P
98US-0090041P
98US-0090042P
98US-0090042P
98US-0090043P
98US-0090043P
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98US-0090043P
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98US-0090079P.
98US-0090080P.
98US-0111715F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BL, Shankara
                                                                                                                                                                                                                                                                                                                                                                                                           GENZYME CORP. ROBERTS B L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHANKARA S.
19 - JUN - 1998;
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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19-JUN-1998;
19-JUN-1998;
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(ROBE/)
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DB 1; Length 10; 1; Indels

42.0%; Score 8.4; DB 90.0%; Pred. No. 95; :ive 0; Mismatches

Conservative

Query Match Best Local Similarity Matches 9; Conserv

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Tue Jun 8 12:32:42 2004
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GENZYME
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
                                                                                                        SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
                                                                                             Human dendritic cell SAGE tag, SEQ ID NO:17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 63; 130pp; English
                                                                                                                                                                                               98US-0089831P

98US-0089844P

98US-0089878P

98US-0089991P

98US-00899997P

98US-00899997P

98US-00899997P

98US-00899997P

98US-0090036P

98US-0090041P

98US-0090041P
                                                     AAZ77589 standard; DNA; 10 BP.
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts BL, Shankara S;
                GCTGGCAGGC 10
        GCTGGCACGC 18
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                                                                                                                                                                                                                                                                                                                                                                                                        (GENZ ) GENZYME COR!
(ROBE/) ROBERTS B L
(SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                             19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                                                                                                                                            Homo sapiens
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                                                                                10-APR-2000
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                                                                   AAZ77589;
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                                                                                                                                                                                                                                                                                        -NO.
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                                         RESULT 83
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expression) tags used to identify many transcripts encoting appression) tags used to identify many transcripts encoting to immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while preferentially or differentially expressed in dendritic cells, while confort transcripts correspond to novel genes. Antigen-presenting cell (APC) -associated costimulatory factors play an important role in the cell varion of the cytotoxic immune response, particularly against tumour antigen presentation via the MMG (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse complex) and subsequent recognition by T-cell receptors is alone for the tumour calls, immunostimulatory coffectors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce a numnum response, particularly capanosis and monitoring of diseases related to abnormal expression of their encoded proteins, can be used to identify expression of their encoded proteins can be used to active immunotherapy (or to stimulate production of a containing them are used in active immunotherapy (or to stimulate production of active immunotherapy. Co-administration of tumour antigen and expression of co-stimulatory factors ensures adequate antigen containing containing the presentation of o-stimulatory signals, migration of chemce of immune effector cells experience of them are used in gene therapy. Co-administration of co-stimu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metastatic breast tumour cell downregulated transcript tag #5125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
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98US-0089997P.
98US-0090039P.
98US-0090040P.
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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B L.
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19-JUN-1998;
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                                                                                AAZ83491;
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                                                                          RESULT 85
                                                                            AAZ8349
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98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P.

99WO-US013647

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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                      Claim 1; Page 132; 219pp; English.
                                                                                               BL, Shankara
(GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.
                                                                                                                                                                                                                                            treatment of cancer.
                                                                                                                                        WPI; 2000-106079/09.
                                                                                                 Roberts
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AAZ85754/c
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                                                                                                                                                                                                                                                                                   that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ8942 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or incomplete transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for disquosis, prognosis, monitoring and transcripts can be used for disquosis, prognosis, monitoring and transcripts can be used for disquosis, prognosis, monitoring and transcripts are immunoasanys or hybridiaetion/amplification reactions. Or seful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Porpeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic additions that produce the polypeptides can be used to expand and isolate populations of educated, antigen-epecific immune effecter
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                                                                                                                                                Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                  Claim 1; Page 195; 219pp; English.
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                                                           Roberts BL, Shankara S;
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                                                                                                                                                                                                      treatment of cancer,
                                                                                                       WPI; 2000-106079/09
          (SHAN/) SHANKARA S.
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AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cella). AA28342 tissue (i.e. are upregulated in metastatic breast tumour cella). AA2863742 to AA286577 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tells). These tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially cuseful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of particularly an antigen encoded by the transcripts are also useful in cacines for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter calls, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
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Pred. No. 95;
0; Mismatches
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98US-0089997P.
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98US-0090040P.
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Best Local Similarity 90.vv,
Best Local Similarity
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Hashimoto S, Matsushima K, Suzuki T;
           (NISC-) JAPAN SCI & TECHNOLOGY CORP.
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                                                                                                                                                                                                                                                                                     that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA28942 tissue (i.e. are upregulated in metastatic breast tumour cells). AA28942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts are metastatic) breast cancer, while promoters from the transcripts are used to direct expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, and these used for adoptive cells.
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                                                                                                                                                                              Isolated polynuclectides differentially expressed between metastatic non-metastatic breast cancer cells, useful for diagnosis, prevention treatment of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.0%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 95; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Claim 1; Page 191; 219pp; English.
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AAA56201/C
XX
AC AAA56201;
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DT 07-SEP-2000 (first entry)
XX
KW Human monocyte gene Tag oligonuc
XX
KW Human, monocyte, macrophage; GM-
XW GM-CSF; identification; diagnosi
KW GM-CSF; identification; diagnosi
KW GM-CSF; identification; diagnosi
KW MO200024892-A1.
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PN WO20024892-A1.
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PN WA200024892-A1.
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PN X28-OCT-1999; 99WO-JP005982.
XX
PR 28-OCT-1999; 99JP-00307532.
 98US-0090041P.
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Best Local Similarity 90...
Best Local 9; Conservative
                                                                                                             Roberts BL, Shankara S;
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                                 GENZ ) GENZYME CORP.
ROBE/) ROBERTS B L.
SHAN/) SHANKARA S.
                                                                                                                                            WPI; 2000-106079/09
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 19-JUN-1998;
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frequently in human monocytes. The CDNA of each game has a sequence fully defined in the specification, and lacking the CATG sequence located defined in the specification, and lacking the CATG sequence located adjacent to polyA region. Also described are: (1) an antibody specifically for the protein encoded by any of the genes; (2) oligonuclectides obtained from the cDNA sequences; (3) 380 human genes colory-stimulating factor, from human monocytes by granulocyte-macrophage colony-stimulating factor, the CDNA of each gene has a fully defined sequence, given in the specification, lacking the base sequence CATG located most closely to the CDNA region; (4) an antibody specifically for the protein encoded by any of the genes of (3); and (5) oligonuclectides obtained from the cDNA sequences of (3). The genes and cDNAs, are used for the study of gene specificially and disease onset mechanism e.g. oncogenesis, genetic diseases, drug development and diagnosis. AAA56107 to AAA56586 represent specifically claimed oligonuclectides sequences for human genes expressed in monocytes and macrophages
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                                                                                                                                                                                                                                                                  The present invention describes 100 human genes, which are expressed most
                                                      Genes most frequently expressed in human monocytes and GM-macrophages M-macrophages studied and with cDNAs characterized, for study of gene specificity, disease onset mechanism, drug development and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                    Claim 1; Page 58; 138pp; Japanese.
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Matches 9; Conservative
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WPI; 2000-350734/30
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19-VUU-61 19-JUN-1

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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161.

AH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
                                                                                                      Human; transcriptome; gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
                                                            Human ubiquitously expressed transcriptome sequence SEQ ID NO: 406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human normal hepatocyte expression gene cDNA, SEQ ID NO: 2.
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                      20-SEP-2001 (first entry)
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Best Local Similarity 90.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /elculescu VE,
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                                                                                                                                                                                                                                 WO200138577-A2.
                                                                                                                                                                                      ното заріеля
                                                                                                                                                                                                                                                                                                                                                                           24-NOV-1999;
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                                                                                                                                                                                                                                                                            31-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts which are differentially expressed in a variety of normal or malignant cell types. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in that particular cell type, while other transcripts correspond to novel genes. The invention also provides a nucleotide comprising a promoter sequence derived from one of the foreign nucleotide sequence, and gene delivery vehicles and host cells comprising the polynucleotides of the invention. A nucleotide comprising the polynucleotides of the invention. A nucleotide comprising the polynucleotides of the invention. A nucleotide comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures to comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures to characterise a cell of a specific tissue type and to determine whether it is normal or malignant. They may be used to screen for agents that modulate expression of differentially expressed genes compound. The promoter foreign gene construct of the invention may be used for example, a promoter derived from a gene preferentially expressed in cargetted expression of the foreign gene in a particular cell type. For example, a promoter derived from a gene preferentially expressed in sequence encoding an antigen. Such a construct could be transduced into the construct could be used to the construct could be transduced into the construct could be used to the construct could be used to the construct could be transduced into the construct could
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune effector cells in vivo, or in cancer immunotherapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide useful in cancer immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 95;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 61; 97pp; English
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                                                                                                                                                                                                                                 98US-0090045P.
98US-0090047P.
98US-0090072P.
98US-0090077P.
98US-0090077P.
98US-0090078P.
98US-0090078P.
                      98US-00900000P.
98US-0090035P.
98US-0090036P.
                                                                                          98US-0090039P.
98US-0090040P.
98US-0090041P.
                                                                                                                                                             98US-0090042P.
98US-0090043P.
98US-0090044P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roberts BL, Shankara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GACTCGCTGG 13
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-106132/09.
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Best Local Similarity
Matches 9; Conserv
                                                                                          19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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19-JUN-1998;
19-JUN-1998;
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AAH63566/CID AAH63XX RESULT 89

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WPI; 2001-629566/73

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The present invention describes an isolated DNA molecule comprising a coding sequence of a year gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                       The invention relates to a human normal hepatocyte expression gene group comprising 200 genes in the human normal hepatocyte. The cDNA of each gene comprises one of 200 fully defined nucleotide sequences as given in the specification. The gene group and the cDNAs corresponding to each of the genes in the group are useful in the diagnosis and treatment of human hepatopathy. The present sequence is a cDNA corresponding to a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression; antifungal; tag; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8333.
                                                                                                                                                                                                                                                                              Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                                     Human normal hepatocyte expression gene group
                                                                                                                                                                                                                                          expressed by normal human hepatocytes
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                                                                                       Claim 1; Page 6; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF41594 standard; DNA; 10 BP
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                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
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Kinzler K;

the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comparising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; (2) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and conting expression in the yeast cell of at least 1 NORF gene whose cervices of the class of drugs. The NORF genes may be used expression is affected by the class of the cell cycle, the differentially control and affect phases of the call cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. Appliable to AAPA964 crepresent SAGE tags used in the exemplification of the present invention.

CAAPA33261 to AAPA3267 represent invention of the present invention. The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatities C (GH) liver tissue or hepatities C-induced the paparocellular carcinoma (HCC) compared with normal human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides polyh region of CDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular call types. The invention also relates to proceins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss. Gaps Chronic hepatitis C/HCC differentially expressed gene SAGE tag #567. Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes. ö 42.0%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 95; ive 0; Mismatches 1; Indels Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other; (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN Claim 46; Page 26; 139pp; Japanese. ABV84757 standard; cDNA; 10 BP 19-JAN-2001; 2001JP-00012328 19-JAN-2001; 2001JP-00012328 9; Conservative 6 CTCGCTGGCA 15 70 WPI; 2002-631294/68. Best Local Similarity Matches 9; Conser JP2002209591-A 12-DEC-2002 Homo sapiens 30-JUL-2002 ABV84757; Query Match RESULT 92 ABV84757 ò 셤

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Mismatches

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42.0%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 95;

hepatocellular carcinoma compared with normal liver tissue

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Score 8.4; DB 1; Length 10; Pred. No. 95; 0; Mismatches 1; Indels

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the expression of groups of genes that are overexpressed in chronic hepatitis C liver tissue or HCC. Groups of genes differentially expressed in chronic hepatitis C tissue or HCC may be used for the diagnosis and treatment of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV84691-ABV84790 are SAGE tags representing the 100 least highly expressed genes out of those genes which are underexpressed in hepatocellular carcinoma compared with chronic hepatitis C liver tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human chronic hepatitis C tissue expression exasperating gene group
comprises 100 high-ranking genes.
                                                                                                                                        Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                             Human HCC underexpressed gene SAGE tag #352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                           ABV84542 standard; cDNA; 10 BP.
                                                                                                                                                                  Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative C
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                                                                                                                                                                                                                          2 TGGACTCGCT 11
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the inventing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C-induced human chronic hepatitis C (CH) liver tissue or hepatitis C-induced human chronic hepatitis C (CH) liver tissue or hepatitis C-induced human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides consist of a sequence of 10 nucleotides consist of a sequence of 10 nucleotides consist of a variety of genes tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also celles to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis C tissue or HCC groups of genes differentially expression to these diseases. Such genes, inhibitors of their expression creatment of these diseases. Such genes, inhibitors of their expression creatment of these diseases. Such genes, inhibitors of their expression carvity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV8450 are SAGE tags representing the 100 least highly invention relates to SAGE (serial analysis of gene expression) ABV84491-ABV84590 are SAGE tags representing the 100 least hig expressed genes out of those genes which are underexpressed in Claim 28; Page 20; 139pp; Japanese

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42.0%; Score 8.4; DB 1; Length 10; ilarity 90.0%; Pred. No. 95; Conservative 0; Mismatches 1; Indel8

Query Match Best Local Similarity Matches 9; Conserv

Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chromic hegatitis C (CH) liver tissue or hepatitis C-induced in human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides content expected downstream of the 5'-CATG-3' sequence motif lying nearest to the polyh region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis C liver tissue or HCC (aroups of genes differentially expressed in chronic hepatitis C liver tissue or HCC may be used for the diagnosis and treatment of these diseases. Such genes inhibitors of their expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences apply expressed in expression or activity, and antibodies against the gene products may be used in the expression or activity, and antibodies against the gene products may be used in the average and antibodies against the gene products may be used in the expression or activity, and antibodies against the gene products may be used in the expression or activity and antibodies against the gene products may be used in the expression or activity.
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                                                                                          Gaps
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hepatocellular carcinoma compared with normal liver tissue
                                          Score 8.4; DB 1; Length 10;
Pred. No. 95;
0; Mismatches 1; Indels
Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human apolipoprotein A-I SAGE tag #315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 28; Page 19; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                         ABV84505 standard; cDNA; 10 BP.
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                                          42.0%;
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                           Query Match
Best Local Similarity 90.v.
Best Local 9; Conservative
                                                                                                                                            2 TGGACTCGCT 11
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ABV84505
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SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss.
                                                                                                                                                                                                                       Human chronic hepatitis C tissue expression exasperating gene group
comprises 100 high-ranking genes.
                                                            Human apolipoprotein A-I SAGE tag #520.
                                                                                                                                                                                         (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN,
                                                                                                                                                                                                                                               Claim 46; Page 25; 139pp; Japanese
              ABV84710 standard; cDNA; 10 BP
                                                                                                                                                                         19-JAN-2001; 2001JP-00012328.
                                            (first entry)
                                                                                                                                                                                                        WPI; 2002-631294/68
                                                                                                                           JP2002209591-A
                                             12-DEC-2002
                                                                                                                                          30-JUL-2002
                             ABV84710;
RESULT 95
ABV84710
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chromatch departitis (CH3) liver tissue or hepartitis C-induced human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides clocated downstream of the S'-CATG-3' sequence motif. Tying nearest to the polyh region of the S'-CATG-3' sequence motif. Tying nearest to the polyh region of the S'-CATG-3' sequence motif. Tying nearest to the polyh region of the Street from a variety of genes . These tags serve to uniquely identify each transcript and can thus be used to analyse the partice of pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the chronic hepatitis C liver tissue or HCC may be used for the diagnosis and in chronic hepatitis C liver tissue or HCC may be used for the diagnosis and creativity, and antibodies against the gene fare the diagnosis and creativity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABVEG-691, ABV84451-ABV84790 are SAGE tags representing the 100 least highly expressed genes out of those genes which are underexpressed in hepatocellular carcinoma compared with chronic hepatitis C liver tissue

Seguence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

42.0%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 95; tive 0; Mismatches 1; Indels Conservative Local Similarity
les 9; Conserv Query Match Best Loca Matches

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RESULT 96 ABV84791 ID ABV84

ABV84791 standard; cDNA; 10 BP

SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;

Human apolipoprotein A-I SAGE tag #729.

12-DEC-2002

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The invention relates to SAGE (serial analysis of gene expression) tags crepresenting groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C-induced hepatocellular carcinoma (HCC) compared with normal human liver tissue. The SAGE tags of this invention consist of a sequence of 10 mucleotides C the SAGE tags of this invention consist of a sequence of 10 mucleotides C polyA region of CDNA region of CDNA derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also c relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic c hepatitis C liver tissue or HCC. Groups of genes differentially expressed in chronic hepatitis C tissue or HCC. Groups of genes differentially expressed in chronic decelopment of these diseases. Such genes, inhibitors of their expression c ractivity, and antibodies against the gene products may be used in the ABV84191-ABV841990 are SAGE tags representing 100 genes which are highly expressed in chronic hepatitis C liver tissue
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                                                                                                                SAGE tag; serial analysis of gene expression; human; chronic hepatitis C_i CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC_i
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.0%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 95;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN,
                                                                                   Human apolipoprotein A-I SAGE tag #601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 55; Page 28; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV84919 standard; cDNA; 10 BP
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                                                   12-DEC-2002 (first entry)
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                        expression pattern; ss.
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Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes.
                                                               (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                          19-JAN-2001; 2001JF-00012328
                                                     .9-JAN-2001; 2001JP-00012328
 expression pattern; ss.
                                                                          WPI; 2002-631294/68
                     JP2002209591-A
           Homo sapiens
                                30-JUL-2002
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human charactise (CH) liver tissue or hepatitis C-induced to hepatocellular carcinoma (HCC) compared with normal human liver tissue.

The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CAPTG-3' sequence motif lying nearset to the polyh region of the 5'-CAPTG-3' sequence motif lying nearset to the polyh region of cDNAs derived from a variety of genes. The invention also calates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes there expressed in chronic hepatitis C liver tissue or HCC (Groups of genes differentially expressed in chronic hepatitis C liver tissue or HCC (Groups of genes differentially expressed in chronic hepatitis C liver tissue or HCC (Groups of genes differentially expressed in chronic hepatitis C liver tissue or HCC (Groups of genes differentially expressed in chronic hepatitis C liver tissue or HCC (Groups of genes differentially expressed in chronic hepatitis C liver tissue or HCC (Groups of genes differentially expressed in chronic hepatitis C liver tissue or HCC (Groups of genes differentially expressed or cractivity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences C ABVM8491-ABVM8490 mas EAGE tags representing 100 genes which are highly considered in the care of the constant of the care of the constant of the care chronic hepatitis C and/or HCC. Sequences and the care and the care of the care Score 8.4; DB 1; Length 10; Pred. No. 95; 0; Mismatches 1; Indels Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other; expressed in hepatocellular carcinoma Claim 64; Page 30; 139pp; Japanese. 42.0%; Query Match
Best Local Similarity 90.00
9; Conservative TGGACTCGCT 11

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Gaps
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TGGACGCGCT 10 원

ABN88036 standard; DNA; 10 BP ABN88036;

Human SCYB14 preferred oligonucleotide detection primer SEQ ID NO:35. Human, small inducible cytokine subfamily B member 14; SCYB14; SNP; single nucleotide polymorphism; polymorphic; platelet aggregation; antiinflammatory; primer; 88.

(first entry)

12-AUG-2002

Homo sapiens

WO200229108-A1.

11-APR-2002

04-OCT-2001; 2001WO-US031303

04-OCT-2000; 2000US-0238101P.

GENA-) GENAISSANCE PHARM INC.

Sausker EA Russo DP, Choi JY,

WPI; 2002-315864/35

New small inducible cytokine subfamily B (Cys-X-Cys), Member 14 (SCYB14) gene polymorphic variants, for studying the expression and function of SCYB14 and screening candidate drugs for treating disorders involving inflammatory responses.

Claim 17; Page 14; 73pp; English.

The present invention describes genetic variants of the human small inducible cytokine subfamily B (Cyg-X-Cyg), Member 14 (BRAK) (SCYB14) canducible cytokine subfamily B (Cyg-X-Cyg), Member 14 (BRAK) (SCYB14) canducible cytokine subfamily B (Cyg-X-Cyg), Member 14 (BRAK) (SCYB14) corresponded to SCYB14 in studying the effect of SCYB14, in expressing SCXB14 protein for use in screening for candidate drugs to creat diseases related to SCYB14 activity, in studying the effect of the creation on the biological activity of SCYB14, and the binding affinity of candidate drugs targeting SCYB14 for the treatment of disorders involving inflammatory responses. Haplotyping methods from the present involving inflammatory responses. Haplotyping methods from the present contenting a specific condition or disease predicted to be associated with SCYB14 activity, or in the design of clinical trials of candidate drugs correcting a specific condition or disease sessificated with SCYB14 activity, Transgentc animals are useful for studying expression of the corrected against SCYB14 protein, and for testing the efficacy of therapeutic agents and compounds for disorders related to platelet against SCYB14 protein, and for testing the efficacy of therapeutic agents and compounds for disorders related to platelet agagregation in a biological system. The present sequence represents a preferred oligonucleotide detection primer for the human SCYB14 gene

Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

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Gaps
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0
DB 1; Length 10;
                    1; Indels
   Score 8.4; DB
Pred. No. 95;
0; Mismatches
   42.0%;
             Similarity 90.0
9; Conservative
     Query Match
Best Local S:
                      Matches
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CICGCIGGCA 15 CICGCICGCA 1 ø

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ACA94471 standard; DNA; 10 BP (first entry) 18-JUL-2003 ACA94471; ACA94471

DNA tag from human transcript elevated in adenomas/cancers #52

Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase; macrophage inhibitory cytokine; MIC; RDP; faeces; blood; kidney proximal tubule.

Homo sapiens.

WO2003022863-A1.

20-MAR-2003

09-SEP-2002; 2002WO-US028518

2001US-0317494P. 2002US-0383805P. 07-SEP-2001; 30-MAY-2002; (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

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Buckhaults P, Kinzler KW, Vogelstein B;
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WPI; 2003-313220/30.

Detecting colorectal cancer in a subject, involves detecting macrophage inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood

Disclosure; Page 26; 59pp; English.

The invention relates to detecting CC (colorectal cancer e.g. colorectal adecoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC) or renal dispeliase (RDP) in faceses or blood of a subject and comparing amount of MIC or RDP detected to that in normal subjects, where an elevated amount of MIC or RDP detected to that in normal subject; (b) isolating mRNA sample from facese of a subject, detecting MIC or RDP mRNA in the mRNA sample and comparing amount of MIC or RDP mRNA in the subject is an indicator of CC in subject; (c) r RDP mRNA in the subject is an indicator of CC in subject, (d) corresponded amount of MIC or RDP mRNA in the mRNA sample to amounts of MIC or RDP mRNA in the mRNA sample to amount of MIC or RDP mRNA in the subject is an indicator of CC in subject, with sample to amount of MIC or RDP mRNA in the subject of a subject, isolating an mRNA cample to amount of MIC or RDP mRNA in the subject; (d) contacting blood or faces of a subject, with the mRNA sample to amount of MIC or RDP mRNA in the subject, detecting activity of RDP in the blood or faces by detection of increased reacting activity of RDP in the blood or faces by detection of increased reacting activity of RDP in the blood or faces by detection of increased reacting activity of RDP in the blood or faces by detection of increased reacting activity of RDP in the blood or faces by detecting activity of RDP in blood or faces by to that in normal subject where an elevated amount of activity of RDP in the blood or faces of the subject is an indicator of CC in the binds to RDP or an inhibitor of RDP where the antibody or inhibitor is comparing the moiety which is detectable from outside of the subject and area of localisation of the moiety within the subject but outside the comparing in the faces or blood RDP reaction product or RDP substrate consulting in the faces or blood PDP reaction product or RDP substrate or an undertained reacting olderived from a man are assigned with the detectable moiety, where increased product or decrease

Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Gaps . 0 Query Match
42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 1; Indels

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11 TGGCACGCAC 20

TGCCACGAAC 1

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ACA94472 standard; DNA; 10 BP. ACA94472;

18-JUL-2003 (first entry)

DNA tag from human transcript elevated in adenomas/cancers #53.

Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase; macrophage inhibitory cytokine; MIC; RDP; faeces; blood; kidney proximal tubule.

Homo sapiens

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The invention relates to detecting CC (colorectal cancer e.g. colorectal adenoma), comprising: (a) detecting macrophage inhibitory cytckine (MIC) or contraining (a) detecting macrophage inhibitory cytckine (MIC) or contraination of MIC or RDP detected to that in normal subjects, where and comparing amount of MIC or RDP detected to that in normal subject; of a subject, detecting MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP mRNA in the subject is an indicator of CC in subject; (b) isolating mRNA sample, and comparing there an elevated amount of MIC or RDP mRNA in the mRNA sample and subject or epithelial cells, detecting an mRNA sample from facese of a subject or epithelial cells, detecting an mRNA sample from facese of a subject or epithelial cells, detecting an indicative of CC in the mRNA sample to amounts of MIC or RDP mRNA in normal subject; (d) contacting blood or faces of a subject, where an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative of CC in the subject; (d) contacting blood or faces of a subject, with a mRDP substrate, detecting activity of RDP in the blood or faces by detection of increased reaction product or decreased RDP substrate, and comparing the amount of activity of RDP in the blood or faces by detecting the amount of activity of RDP in the blood or faces of the subject and cativity of RDP in the blood or faces of the subject in the blood or faces of the subject is an indicator of CC in the subject in the blood or faces of the subject and detecting the moiety which is detectable from outside of the subject and activity of RDP in the subject where an elevated of the subject where an elevated or the subject where an elevated or the subject where an elevated in the faces or blood or faces or blood or faces or blood by the subject or decreable moiety, where increased product or decreased with the detecting certable moiety, where increase
                                                                                                                                                                                                                                                                                                                               Detecting colorectal cancer in a subject, involves detecting macrophage inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood of the subject.
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                                                                                                                                                                                                                                                       Buckhaults P, Kinzler KW, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 26; 59pp; English.
                                                                                         2002WO-US028518.
                                                                                                                                    07-SEP-2001; 2001US-0317494P.
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WO2003022863-A1.
                                                                                         09-SEP-2002;
                                            20-MAR-2003
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Gaps . 0 Match .42.0%; Score 8.4; DB 1; Length 10; Local Similarity 90.0%; Pred. No. 95; ly Conservative 0; Mismatches 1; Indels Query Match Best Loca Matches

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11 TGGCACGCAC 20

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10 TGGCACGAAC 1

AAQ85812/c ID AAQ85812 standard, DNA, 11 BP. AAQ85812; RESULT 101 SXXX

Synthetic.

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The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying markers of skin ageing and/or stress; (MI) is skin ageing and/or stress; and identifying or determining the effects of skin ageing and/or stress; and identifying or determining the effects of sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                        Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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Pred. No. 1e+02;
0; Mismatches 1; Indels
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Similarity 90.0%;
9; Conservative
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Best Local Similarity
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                 Homo sapiens.
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Matches
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                                                                                                                                                                                                                                                        /noce= noptionally 5'-O-(dimethoxytrityl)-2'-O-[hexyl-
(omega-N-phthalimidoamino)-, 2'-O-hexyl-N-(1-pyvene-
propyl-carbonyl)amino-, 2'-O-[6-bromoacetamido-hexyl]-,
or 2'-O-[hexyl-N-(polyethylene glycol)-propionoyl]- amino

    useful as

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New amine-derivatised nucleoside(s) and oligo:nucleoside(s) - useful as
diagnostics, therapeutics and research reagents, partic. in anti-sense
                                                                                 Alkylamino group; ribofuranosyl sugar; antisense therapy; virus; HIV; herpes; papilloma; antiviral; ss.
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                                                       2'-0-alkylamino-containing oligomer #52
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                                                                                                                                                                                     Location/Qualifiers
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(revised)
(first entry)
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les 9; Conser
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modified_base
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25-MAR-2003
07-NOV-1995
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Cook PD,

therapy.

Query Match

Matches

ABQ86878,

RESULT 102

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Gaps

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sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention

Seguence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

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XEFFXXXCCCCCCCCXXX
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                                                                                                                                                                                                                                              The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from expression. (A) comprises protein or mRNAs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmacoutical or comentic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential
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                                                                                                                                                                         Claim 8; Page 51; 325pp; German.
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                                                    TGGCGCGCAC 11
Local Similarity
les 9; Conserv
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            Matches
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10-SEP-2002 AB087015

Human skin stress/ageing related EST SEQ ID NO 770.

Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

WO200253773-A2. Homo

11-JUL-2002

20-DEC-2001; 2001WO-EP015178

03-JAN-2001; 2001DE-01000121

(HENK) HENKEL KGAA

Hofmann Σ Conradt Petersohn D,

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WPI; 2002-528865/56.

gene Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential expression

Claim 8; Page 69; 325pp; German.

The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (M1) is usefful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present

RESULT 106 ABQ87551

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screening for cosmetic or therapeutic agents, based on differential gene
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       42.0%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 1e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                            Human skin stress/ageing related EST SEQ ID NO 676.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hofmann K;
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                                                                                                                                                                         ABQ86921 standard; cDNA; 11
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Best Local Similarity 90.0.
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Query Match
Best Local Similarity 90.v.
Pest Local 9; Conservative
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                                                                     3 GGACTCGCTG
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ABQ87551

11-JUL-2002

expression.

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; sumburn; psoriasis; scleroderma; rosaccea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
                                                                                                                                                                                                                                  In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 BP, 3 A, 3 C, 4 G; 1 T; 0 U; 0 Other;
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                                     20-DEC-2001; 2001WO-EP015179
                                                                               03-JAN-2001; 2001DE-01000127
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                                                                                                                      (HENK ) HENKEL KGAA
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11-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                           Human skin stress/ageing related EST SEQ ID NO 1306
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  CDNA; 11
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Best Local Similarity 90.0
Matches 9; Conservative
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  ABQ87551 standard;
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                                                                                                                                                                                                            Homo sapiens.
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In vitro identification of skin-expressed genes, useful for determining

WPI; 2002-590638/63

WO200253774-A2

Homo sapiens

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ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of skin. The present sequence is that of a human expressed sequence tag (ESI) of the invention

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Sequence 11 BP; 1 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression ($AGE) (M1) is useful for identifying genes involved in skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis, atopbic dermatitis, acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                        Claim 24; Page 289; 1345pp; German.
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Best Local 9; Conservative
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                      e.g. skin cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Score 8.4; DB 1; Length 11; Pred. No. 1e+02; 0; Mismatches 1; Indels
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   42.0%;
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The invention relates to in vitro identification (W1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basel cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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90.0%;
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ABV71048
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sumburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis, acne, seborrhea; lupus ertythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
Human, skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Best Local Similarity 90.0
Matches 9; Conservative
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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                                                                       Claim 24; Page 271; 1345pp; German.
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Best Local Similarity 90.00
Best Local 9; Conservative
                   Conradt M,
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                                                           e.g. skin cancer.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaas; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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                                                                                                                                                                                 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Pred. No. 1e+02;
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosace; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Pred. No. 1e+02;
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ABV63466 standard; cDNA; 11 BP.
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immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Pred. No. 1e+02;
0; Mismatches 1; Indels
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    Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
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                            In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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WPI; 2002-590638/63
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Seguence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

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determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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"paired with bps 12-7 of hexadecanucleotide no.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ′*tag≃
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                      9 GCTGGCACGC 18
                                                                                                                                                                                                                                                  10
                                                                                               of the invention
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                                                                                                                                                                                                                                                   GCTGGCAGGC
                                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
03-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8500813-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seeman NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                              AAN50511;
                                                                                                                                                          Query Match
                                                                                  skin.
(EST)
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                                                                                                                                                                                Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; ss; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
inflammatories for treating e.g. asthma, Crohn's disease, ulcerative
collitis, diabetes, glomerulomephritis, acute respiratory distress
syndrome and the formation of atherosclerotic plaque
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          composition containing immune stimulant and inhibitor of agent tadversely affects the immune response, for treating cancers and infections.
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                                                                                                                                                                           Immunosuppressant inhibitor oligonucleotide TGF-betal-98-9.
Length 12;
                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                      (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
Score 8.4; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                           Schlingensiepen R,
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Fig 1; 30pp; English.
                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                    99WO-EP004013.
                                                                                                                                                                                                                                                                                                                                                                  98EP-00113974.
                                                                                                                                                                                                                                                                                                                                                        98EP-00110709
 h 42.0%;
Similarity 90.0%;
9; Conservative
                                                                                                                AAZ65521 standard; DNA; 12
                                                                                                                                                        (first entry)
                                          10
                                                             72
                                           1 ATGGACTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                           Schlingensiepen K,
  Query Match
Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                    10-JUN-1999;
                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                                                                                                                                         10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                    25-JUL-1998;
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                                                                                                                                     AAZ65521;
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A. thaliana primer walking octamer SEQ ID NO: 179.

24-NOV-2000 (first entry)

AAA80866;

AAA80866 standard; DNA; 8 BP.

RESULT 124 AAA80866/c

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The invention provides a device, system and method for a programmable finite automaton comprising a biomolecule, such as DNA, and associated biomolecule-manipulating enzymes, that solves computational problems autonomously. The hardware for the automaton preferably includes biomolecule-manipulating enzymes, such as restriction nucleases and ligamese, the software for the automaton preferably includes biomolecule-manipulating enzymes, such as restriction nucleases and ligamese, the software and input are preferably encoded by double-stranded DNA, and programming is preferably perferand by choosing appropriate software DNA molecules. The molecular computing machine uses the free-energy difference between its input and output to accomplish a computation, preferably using its input DNA molecule as a partial or the sole source of energy. It transforms an input DNA molecule into an output DNA molecule by digesting the input as it computes. An exemplary molecule inclease FoxI, 74 DNA ligase and ATP. The software comprised 8 short nuclease FoXI, 74 DNA ligase and ATP. The software comprised 8 short sequence, encoded the initial state of the automaton and the present sequence, encoded the initial state of the automaton and the input. The computation started when the hardware, software and input are mixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Programmable finite biomolecular automaton for performing computation through manipulation of molecules, includes polymeric biomolecule, and biomolecule-manipulating components.
                                      Gaps
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  Length 12;
                                      Indels
Score 8.4; DB 1; Le Pred. No. 1.1e+02; O; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 BP; 1 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paz-Elizur T;
                                                                                                                                                                                                                                                                                                                           Input molecule for molecular automaton.
                                                                                                                                                                                                                                                                                                                                                                Computer; molecular automaton; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adar R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 2; 52pp; English.
                                                                                                                                                                                                           ACC58710 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    together and ran autonomously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-2001; 2001US-0331318P.
07-JUN-2002; 2002US-0386418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-2002; 2002WO-IL000915
42.0%;
ilarity 90.0%;
Conservative
                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                             GAGTCGCTGG 12
                                                                           4 GACTCGCTGG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-482351/45.
Query Match
Best Local Similarity
Matches 9; Conserv.
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                                                                                                                                                                                                                                                                                    26-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                  ACC58710;
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This invention describes a novel method for sequencing an unknown DNA molecule which comprises selecting a library primer from an octamer of digonaclectide library consisting of 48 beb sequences and corresponding complementary sequences, where the library primer is complementary to a known sequence adjacent to the unknown sequence or is complementary to a sequence in a known extension product. The method is useful for DNA nucleotide sequencing, in PCR, and in other processes which make use of primers. The octamers are used to identify coding sequences. Primer walking using the octamer libraries is advantageous over other sequencing methods because it does not require multiple cloning steps nor subsequent template preparations, and it is a directed and methodical approach.

AAA&0688-A8125; represent the octamer primers used in the primer walking
                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing an unknown DNA molecule for the polymerase chain reaction and other primer processes comprises primer walking of octamer oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune gene repertoire; T-cell receptor; TCR; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune gene variable region amplifying TCRB 3' PCR primer.
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                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.0%; Score 8; DB 1; Length 8; 100.0%; Pred. No. 1.2e+03; ative 0; Mismatches 0; Indele
                                                                                              Primer walking; octamer; primer; DNA sequencing; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Col 115-116; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                Homayouni R;
                                                                                                                                                                                                                              97US-00859954.
                                                                                                                                                                                                                                                               96US-00632782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  method of the invention
                                                                                                                                                                                                                                                                                                                                                Hardin SH,
                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                               NOTSUOH VINU (-OHYU)
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-474852/41.
                                                                                                                                                                                                                                                                                                                (HARD/) HARDIN S H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                21-MAY-1997;
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                                                                                                                                                                                                04-JUL-2000.
                                                                                                                                                               US6083695-A.
                                                                                                                                                                                                                                                                                                                                                Hardin PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL60738;
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ID AAL6
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AC AAL6
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KW Huma
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Gaps

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llarity 90.0%; Conservative

Local Similarity les 9; Conserv

Best Loc Matches

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Two primers are used to amplify any given mRNA molecule in its cDNA form. The first primer is capable of binding either to (1) a site immediately upstream of the first adenine nucleotide of the poly A tail; (2) to a site including the mRNA's poly A signal sequence; (3) to a site including the mRNA's poly A signal sequence of an mRNA of which the nucleotide sequence or (4) to a sequence of an mRNA of which the nucleotide sequence the ornesponding cDNA sequence. The second primer comprises an arbitrary sequence and is used alongside the first primer to amplify the cDNA molecule by PCR. This primer is a second arbitrary primer. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIP-1; allograft inflammatory factor 1; transplant rejection; inhibitor; immunogenic; detection; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ99334-Q93396 are primers used to identify DNA from both allogeneic a syngeneic sources to determine where a specific gene is expressed. The AIF-1 gene is a differentially expressed allograft gene which is expressed in allograft tissue during transplant rejection. Identificati of the AIF-1 product (AAR80520) or transcript indicates that allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding allograft rejection factors and immunogenic fragments useful for identifying transplant rejection inhibitors.
                                                                                                                                 Cloning and isolating mRNA as cDNA - by reverse transcription and polymerase amplification using two oligo-deoxy-nucleotide(\theta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Syngeneic and allogeneic transplant comparison primer, OPA-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 12, 138pp; English.
             (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                   Example 4; Page 17; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US014724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TCGCTGGC 14
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                                                         Pardee AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                              WPI; 1993-303488/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09517506-A1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for profiling immune gene repertoire or detecting the presence of a specific immune gene in a vertebrate. The method comprises hybridising the nucleic acid molecules representing the immune gene repertoire, to immobilised objectules. The method is useful for profiling the antibody and T-cell receptor (TCR) mRNA repertoire of an organism, and for detecting the presence of a specific immune gene in a vertebrate. Compounds that increase or reduce the transcription of at least one immune gene, the number of immune receptors and/or the number of immune cells in a vertebrate, are useful for treating an immune disorder. The present sequence is human immune gene variable region amplifying PCR primer consensus sequence. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                               Characterizing immune gene repertoire or detecting the presence of a specific immune gene in a vertebrate, comprises hybridizing the nucleic acid molecules representing the immune gene repertoire, to immobilized oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA; mRNA; primer; PCR; polymerase chain reaction; poly A site; RT; reverse transcriptase; kozak sequence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 9 BP; 1 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
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100.0%; Pred. No. 1e+
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer for production of cDNA from mRNA.
  therapy; immune gene; PCR; primer; ss.
                                                                                                                                                                                                                                                                                      Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ47917 standard; DNA; 10 BP.
                                                                                                                                                              15-NOV-2002; 2002WO-EP012822.
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93US-00033084
                                                                                                                                                                                                       23-NOV-2001; 2001GB-00028153
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(first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                      Gehrmann M, Schwers S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGGCAC 16
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                                                                                                                                                                                                                                             (FARB ) BAYER AG.
                                                                                 WO2003044225-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-1992;
11-MAR-1993;
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                                         Homo sapiens
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23-MAR-1994
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Identification

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Gaps

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homocysteine, hypohomocysteinaemia, atherosclerosis, diagnosis, Dami cell, PCR, arbitrary primer, messenger RNA pool, ss.

are therefore

144/c AAT75144 Btandard; DNA; 10

(first entry)

04-MAR-1998

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Gaps

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AAT75144;

Arbitrary RT-PCR primer

WO9725440-A2

Synthetic.

serum;

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The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which were used along with 4 degenerate 3' oligo dT primers for the differential display of human chondrocyte mRNA by reverse transcription and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA clones, which were then searched against PDNA databases for homology to known human genes. The cDNA mols. can be used for the prodn. of gene specific primers and probes to isolate genes induced by treating (septembran) condrocytes with interlevin-lbeta (IL-lbeta), and for the diagnosis of IL-lbeta related connective tissue diseases, in partic.
                                                                                                                                                                                                                                                                                                                                                                                                                               Differential display of mRNA, reverse transcription, DDRT-PCR, human, chondrovyte; gene specific; primer; probe, isolation, interleukin-lbeta, IL-lbeta, diagnosis; connective tissue disease; oseteoarthritis; rheumatoid arthritis; polymerase chain reaction; ss.
rejection is taking place. The human AIF-1 gene and product are therefor useful in the diagnostic of transplant rejection. The diagnostic methods used allow rejection (vascular inflammation) to be detected at an early stage and require only a small amount of biopsy material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis and treatment of II-1 mediated connective tissue diseases - using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or antibodies to them.
                                                                                                                                                0; Indels
                                                                                                              DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                               Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                 oligodecamer DDRT-PCR primer OPA 16.
                                                                                                             40.0%; Score 8; DB 1
100.0%; Pred. No. 1.2
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 15; 31pp; English.
                                                                                                                                                                                                                                                                                                AAT18616 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95EP-00115510.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                               Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Margerie D;
                                                                                                                                                                              7 TCGCTGGC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-181045/19.
                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARH ) HOECHST AG.
                                                                                                                                                                                                            TCGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                   Arbitrary 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-0CT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                  06-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP705842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bartnik E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                  AAT18616;
                                                                                                                                                                                                                                                                  RESULT 128
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Arbitrary RT-PCR primers (AAT75138-42) were used to amplify mRNA from cells exposed to hyperphysiological, normal or subphysiological levels of homocysteine. PCR products were separated on a sequencing gel and discrete fractions which were increased or decreased were identified. This method was used to identify mRNA and the corresponding cDNA which are increased in the cells of a patient having hyperhomocysteinaemia or a predisposition to homocysteine mediated atherosclerosis. These polymucleotides can be used for the diagnosis and treatment of atherosclerotic diseases and diseases of metabolism of sulphur containing amino acids (e.g. homocysteinaemia), which are associated with vascular damage and atherosclerotic disease, specifically unstable angina, acute myocardial infarction (heart attack), cerebrovascular accidents (stroke), hypertension, renal artery stenosis, acutic stenosis and deep vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                       Methods and polynucleotide(s) for diagnosing hyperhomocysteinaemia -and/or predisposition to develop premature atherosclerosis by detecting increased levels of serum homocysteine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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llarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human breast cancer gene differential display primer #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                  (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 22; 84pp; English
                                                                                                                                                                                                                                                                                                                                                               Weitz J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                     96US-00582261.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                               Hirsh J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGCTGGC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-372877/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 8, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occlusive disease
                                                                                                                                                                                                                                                                       02-JAN-1997;
                                                                                                                                                                                                                                                                                                     03-JAN-1996;
                                                                                                                                                                                                                                           17-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1998
                                                                                                                                                                                                                                                                                                                                                               Austin RC,
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Matches
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AAV10688
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Gaps ö

0; Indels

40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 8; Conservative

TCGCTGGC 14

7

8

TCGCTGGC

12:32:42 2004

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Tue Jun

16-OCT-1997

Smith H,

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PCR primers AAV15590 and AAV15591 are used to amplify fragments of the C4.8 and C21.7 genes from a human papillomavirus (HPV) immortalised human forestin keratinocyte cell line HPK-1A. These genes are characteristic of late or early passage cells can be used in a method for assessing the potential for progression of cervical lesions. Antibodies generated against the encoded polypeptide are used for diagnosis of cervical cancer and to assess potential for lesion progression. Antibodies can also be used therapeutically by inhibiting the polypeptide. Antisense molecules based on the nuclectide sequence are used to inhibit expression of the protein. Detecting polypeptides, or related RNA, characteristic of late passage cells (which are potentially malignant) in cervical smears is a reliable way of assessing progression potential
                                                                                           Nucleic acid characteristic of late or early passage cells immortalised by papilloma virus - and related polypeptide(s) and antibodies, used for diagnosis and treatment of cervical cancer and assessing potential for progression of cervical lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast, Saccharcmyces cerevisiae; transcriptome; cell cycle; regulation; eukaryotic cell; antifungal; SAGE tag; gene expression; serial analysis of gene expression; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast transcriptome - useful for modulating eukaryotic cell, for screening antifungal agents, and for identifying genes in cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast tag for additional NORF chromosome 4 tag position 1324367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinzler KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 26; 44pp; English.
                                                                                                                                                                                                        Example 1; Page 4; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV50265 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US001216.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TCGCTGGC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-427943/36.
                                                            WPI; 1998-121623/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 reserese 2
                    Duerst M, Nees M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /elculescu VE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV50265,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primers AAV10683-V10688 are used to obtain novel human breast cancer genes by differential display. The identified genes or fragments of these genes by differential display. The identified genes or fragments of the intimately used for identifying genes and gene products that are intimately related to malignant transformation or maintenance of the screen properties of cancer cells. It can also be used to design or screen disgnostic reagents or therapeutic compounds. Kits are included within the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Breast cancer genes - used to develop products to design or screen diagnostic reagents or therapeutic compounds.
Breast cancer; malignant transformation; diagnostic; therapeutic;
screening; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cervical cancer; treatment; diagnosis; passage cell; lesion; human foreskin keratinocyte cell line; HPK-1A; antibody; smear; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                         (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human HPK-1A C4.8 and C21.7 PCR primer AP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 46; 118pp; English.
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                                                                                                                                                                                                                                                                       96WO-US009286.
96US-0019202P.
96US-00678280.
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ses 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TCGCTGGC 14
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                                                                                                                                                                                                                                                                                                                                                                                                      Chen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE19649207-C1
                                                                                                                                                                                                                                                                       05-JUN-1996;
06-JUN-1996;
11-JUL-1996;
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                                                                                                                                                                                                               09-APR-1997;
                                                                Synthetic.
Homo sapiens
                                                                                                                               WO9738085-A2
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Query Match

Matches

ò d 26-FEB-1998

Synthetic

AAV15590;

RESULT 131

AAV15590/

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Gaps

.; 0

Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

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Teast transcriptome is encoded by a DNA molecule comprising a yeast gene involved in cell cycle progression selected from the group of nonannotated GRF (MORE) genes. SAGE (serial analysis gene expression) tags for highly expressed genes and NORF genes are given in AAV50051 to AAV50345. The present invention describes: (1) a method of using yeast genes to modulate the cell cycle which comprises administering to a cell or isolated DNA molecule comprising a yeast gene which is involved in cell cycle progression selected from differentially expressed genes (SAGE tags given in AAV50051 to AAV50345); (2) a method for screening candidate antiturgal drugs which comprises contacting a test substance with a yeast cell and monitoring expression of a yeast gene which is involved in cell cycle progression; (3) a method of identifying human genes which are circled cycle progression which comprises hybridizing a probe comprising at least 10 contiguous nucleotides of a yeast gene which is differentially expressed between at least 2 phases selected from the log the phase in the cell cycle, where the probe for ascertanning the phase in the cell cycle, where the probe comprises the last 1 contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to AAV50345), or as an array of probes on a solid support
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Brassica napus nucleic acid and protein, useful for regulating dehiscence and/or plant abscission by producing transgenic plants opropagating material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer for DNA encoding a dehiscence zone protein ORS7(9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dehiscence zone protein, ORS7(9); regulation; pod dehiscence;
plant abscission; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 40.0%; Score 8; DB 1; Length 10; Local Similarity 100.0%; Pred. No. 1.2e+02; nes 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paul W, Roberts JA, Whitelaw C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-GB002836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX34945 standard; DNA; 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 GCACGCAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 GCACGCAC 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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PCR primer AAX34944-45 were used to amplify DNA encoding a dehiscence zone protein designated ORS7(9). The ORS7(9) polymucleotides and polypeptides are useful for regulating pod dehiscence and plant abscission. Antisense ORS7(9) nucleic acid useful for preventing or

reducing dehiscence or abscission

Example 1; Page 10; 20pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus)
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                        Gaps
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0
                                                                                                                                                                                                                                  protein; dehiscence; male sterile plant; oilseed rape; primer; ss.
DB 1; Length 10;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer AP-1 used to amplify Rin2 cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
40.0%; Score 8; DB 1
100.0%; Pred. No. 1.2
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        Whitelaw
                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX26829 Btandard; DNA; 10 BP.
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                                                                                                                                     AAZ22961 standard; DNA; 10
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                          8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               (BIOG-) BIOGEMMA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                        Roberts JA,
                                                 7 TCGCTGGC 14
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                                                                                                                                                                                                                                                   shatter resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-580449/49.
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                                                                        9 rcdcrddc 2
                                                                                                                                                                                                                                     Signal transduction
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Best Local Similarity
                                                                                                                                                                                                             Arbitrary primer A.
             Local Similarity
                                                                                                                                                                                                                                                                                                WO9949046-A1.
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                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                              AAZ22961;
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  Query Match
              Best Loca
Matches
                                                                                                            RESULT 134
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The present invention describes nucleic acids comprising human, murine or rat cDNAs encoding DRM proteins (derived from the down-regulated in v-mos crat cDNAs encoding DRM proteins (derived from the down-regulated in v-mos cuseful for arresting call growth; The nucleic acids, and DRM proteins, are useful for arresting call growth; Inhibiting tumour cell growth; treating hyperproliferative cellular disorders, either in vivo or ex vivo and producing fusion proteins with enhanced green fluorescent protein (EGFP) of increased stability (useful in screening assays, protein- protein (EGFP) of increased stability (useful in screening assays, protein- protein contenting abnormally low levels of DRM, or the nucleic acids, may be used to identify subjects with an increased risk of developing a contenting primers to detect or quantify drm and to screen genomic and companies and primers to detect or quantify drm and to screen genomic and companies. Antibodies raised against DRM can be used getect/quantify DRM in immunoassays. Fusion proteins of DRM and GFP are consisted to the nucleus (in contrast cytoplasmic localisation of GFP itself) and so are more stable, e.g. on exposure to fixatives or chergents, and thus form more versatile reagents, e.g. they can be used in fluorescence-based assays that require cell fixation, or linked to proteins or antibodies for use in enzyme-linked immunosorbent assays. Stable EGFP can be attached to proteins during synthesis, allowing the content sequence represents a PCR primer for rat DRM
                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding DRM protein, for regulation of cell growth, particularly treating cancer and.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer associated gene; cancer specific gene; C1-9a11-2; CH8-2a13-1; CH13-2a12-1; CH14-2a16-1; cancer; gene duplication; RNA overabundance; breast cancer; lung cancer; glioblastoma; pancreatic cancer; colon cancer; prostate cancer; hepatoma; myeloma; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe used to obtain cancer associated gene cDNA sequences.
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100.0%; Pred. No. 1.2
tive 0; Mismatches
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                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES
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Best Local Similarity luv...
8; Conservative
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                                                                                                                                                           26-MAR-1998;
        709949041-A1
                                                                                                         26-MAR-1999;
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                                                          30-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a primer used to amplify Rin2 cDNA sequences. Rin2 polypeptides downregulate functional responses elicited by Ras-dependent signalling pathways. Agents that increase Rin2 activity (particularly Rin2 itself, optionally expressed from a vector) are used to treat allergy (asthma, hayfever or atopic eczema); Ras-dependent cancers and (non-)neoplastic cellular proliferation; autoimmune diseases, racell-associated diseases and T cell dependent graft vs. host disease (typical examples being type I diabetes mellitus; multiple sclerosis, Crohn's disease, autoimmune hepatitis and psoriasis). Agents that inhibit kin3 activity are used to improve wound healing; anglogenesis and/or respithelialization (also to improve immune response to pathogens; in human immune deficiency virus, and some other, infections; immune suppression associated with cancer therapy, and nerve regeneration)
Rin2; downregulation; functional response; allergy; asthma; hayfever; Ras-dependent signalling pathway; allergy; asthma; hayfever; atopiec cezema; Ras-dependent cancer; meoplastic cellular proliferation; autoimmune disease; T cell dependent graft vs. host disease; type I diabetes mellitus; multiple sclerosis; Crohn's disease; autoimmune hepatitis; psoriasis; wound healing; angiogenesis; re-epithelialization; human immune deficiency virus; immune suppression; cancer therapy; nerve regeneration; PCR primer; ss.
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Gaps ..

Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Local Similarity 100.

Matches

Query Match

7 TCGCTGGC 14

TCGCTGGC 2

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AAZ25357 standard; DNA; 10 BP.

RESULT 136

17-DEC-1999 (first entry)

AAZ25357;

Rat DRM PCR primer #1.

Synthetic. Rattus sp.

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

11-SEP-1997; 02-OCT-1997;

Tam S, Tsai M, Galli SJ;

WPI; 1999-229239/19.

98WO-US019056. 97US-0058520P 97US-00942819

11-SEP-1998; 18-MAR-1999.

WO9913079-A1

Synthetic.

Rin2 polypeptides and related nucleic acid. Disclosure, Page 47; 101pp; English.

8 12:32:42 2004

Tue Jun

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                                                                                                                                                                                                                                                                                                   CDNA sequences. These cancer specific genes are designated C1-9a11-2. CH8 -2a13.1. CH13-2a12-1, and CH14-2a16-1. These genes show RNA overabundance in a mijority of cancer cell lines tested, as well as a gene duplication in many of the cancers. Probes and primers derived from the polymucleotide sequence may be used to measure or detect altered gene duplication or overabundance of RNA in cancerous cells. This allows the screening of cancer, especially breast cancer, by correlating gene duplication of RNA overexpression obtained in this method with an increased risk for cancer. The polymetide, and its antibodies, are used as reagents for detecting altered protein expression in cancerous cells. Both the cancer associated polypeptide and polymucleotide may be used to gene therapy to treat cancers such as lung cancer, fleplastoma, myeloma and pancreatic cancer, colon cancer, prostate cancer, hepatoma, myeloma and
                                                                                                                                                                                                                                                                                         AAZ99299-Z99304 represent probes used to isolate cancer associated gene
                                                                                                                                                                         New cancer associated polypeptides, genes encoding them and antibodies against them, useful for diagnosing breast cancer and screening for anticancer drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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                                                                        (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST. (USGO ) US GOVERNMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human dendritic cell SAGE tag, SEQ ID NO:1287.
                                                                                                                                                                                                                                                            Example 2; Page 87; 154pp; English
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98US-0089853P.
98US-0089878P.
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Best Local Similarity 100.0%;
Warches 8; Conservative 0
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                 99WO-US018101.
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19-JUN-1998;
19-JUN-1998;
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               10-AUG-1999;
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                                                10-AUG-1998;
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Sequences AA277573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding imminostimulatory cofactor proteins which are preferentially or proteins which are preferentially copared differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell of the ottorior city of extractors play an important role in the activation of the Oytoxic immune response, particularly against tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone to the tumour cells, immunostimulatory cofactors also being required for insufficient octivation of cytotoxic Immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic call uses:

CT They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of fiferentially expressed genes in APC; and as hybridistation probes amplification primers for the diagnosis and monitoring of diseases related to abnormal cappens belonging to the monocyte lineage. Cells containing these genes cells as belonging to the monocyte lineage. Cells containing these genes complexion of an APC; and as hybridistion probes and cells and containing the expressed genes complexion of an active containing the expressed genes of the monocyte lineage. Cells containing these genes containing the expression of them are used in gene therapy. Co-administration of tumour antigens and presented to abnormal engagemented of an appearance of the containing tractors engagemented of the monocyte lineage. The production of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
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98US-0089991P.
98US-0089993P.
98US-0089994P.
98US-0089997P.
98US-009003P.
98US-0090040P.
98US-0090040P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHAN/) SHANKARA S.
                                    19-JUN-1998,
19-JUN-1998,
19-JUN-1998,
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19-JUN-1998,
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Claim 1; Page 119; 130pp; English.

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                                                                                                                                                                    SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                                                                                                                              cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; 88.
                        Gaps
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0
     Score 8; DB 1; Length 10;
Pred. No. 1.2e+02;
; Mismatches 0; Indels
                                                                                                                                                    Human dendritic cell SAGE tag, SEQ ID NO:1924.
        Score 8;
40.0%; Scor.
100.0%; Pre
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9805-0089991P.
9805-0089993P.
9805-0089994P.
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                                                                                                   AAZ79496 standard; DNA; 10
                                                                                                                                    10-APR-2000 (first entry)
       Query Match
Best Local Similarity 100.
Matches 8; Conservative
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ROBERTS B L.
SHANKARA S.
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SA-inducible gene; transgenic plant, pathogen resistance; PCR primer; ss.
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                                                                                                                                                                                                                              presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich si secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells
                    Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
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                                                                                                                                                                                                                                                                                                                                                                                                                Primer AP1 to identify tobacco salicylic acid inducible genes.
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                   Score 8; DB 1; Length 10;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                    Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chua N;
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     AAZ50856 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                  TGGCACGC 18
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AAZ50856/c
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18-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ84391;
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                                                                                               The patent discloses fifteen new salicylic acid (SA) inducible genes from Nicotiana tabacum, nine of which were subcloned and sequenced. Based on different kinetics of induction response, these genes were classified into four categories, class I, II, III and IV response genes. The SA-inducible genes are useful for making transgenic plants with enhanced pathogen resistance. The plants incorporating these genes show reduced pathogen resistance. The plants incorporating these genes show reduced primer API used in differential display PCR reactions along with downstream primers T12MG or T12MC to identify tobacco SA-inducible genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotides differentially expressed between metastatic non-metastatic breast cancer cells, useful for diagnosis, prevention
                                      Novel salicylic acid inducible genes from tobacco plants, useful for making transgenic plants with enhanced pathogenic resistance.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, metastatic breast tumour tissue; breast cancer; tag, primer, non-metastatic breast tumour tissue, gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                                                                      40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; cive 0; Mismatches 0; Indels
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                                                                            Example 1; Page 51; 57pp; English.
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98US-0089997P.
98US-0090039P.
98US-0090040P.
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8; Conservative 0
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ROBERTS B L.
SHANKARA S.
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              WPI; 2000-205725/18
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Best Local Similarity
Matches 8; Conserv
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19-JUN-1998;
19-JUN-1998;
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(ROBE/)
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AAZ83127
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tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcripts that are to preferentially transcribed in the primary or non-metastatic breast tumour citissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen specific immune effecter cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen specific immune effecter for immorbace.
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98US-0089997P.
98US-0090039P.
98US-0090040P.
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Best Local Similarity
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that are preferentially transcribed in the metastatic breast tumnour calls of the are preferentially transcribed in the metastatic breast tumnour calls of the are upregulated in metastatic breast tumnour calls of the adagnosis and adagnosis of the area of the area.
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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0; Mismatches
             Claim 1; Page 78; 219pp; English.
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ROBERTS B L.
SHANKARA S.
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(ROBE/) F
(SHAN/) S
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AAZ82875/c
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that are preferentially transcribed in the metastatic breast tumour cells. that are preferentially transcribed in the metastatic breast tumour cells. AA286971 represent tags corresponding to distinct transcripts that are to AA286677 represent tags corresponding to distinct transcripts that are corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These crashed in the primary or non-metastatic breast tumour cells, transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and cranscripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of ceg. therapeutic genes (also ribozymes or antisense sequences), particularly an antisen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antisense or as therapeutic calls that produce the polypeptides or as therapeutic calls. Host cells that produce the polypeptides or as therapeutic calls, e.g. cytotoxic T lymphocytes, and these used for adoptive immunor herapen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; ative 0; Mismatches 0; Indels
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98US-0089997P.
98US-0090039P.
98US-0090040P.
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AAZ81505;

Query Match Best Local Similarity 8, Conserve

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Roberts BL, Shankara

WPI; 2000-106079/09.

(GENZ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.

19-JUN-1998;

WO9965928-A2 Homo sapiens

23-DEC-1999.

18-JUN-1999;

19-JUN-1998; 9-JUN-1998; 19-JUN-1998;

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Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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19-JUN-1998;
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19-JUN-1998;
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells. AAZ83942 tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tells). These tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can modulate expression of the transcripts are potentially compunds that modulate expression of the transcripts are potentially constituted to the transcripts are potentially constituted to the transcripts are potentially of the transcripts are located of larged expression, in selected cell types, of the transcripts are also useful in contines Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                     Claim 1; Page 167; 219pp; English.
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                                                                                                                                                 that are preferentially transcribed in the metastatic breast tumour clistic transcripts that are preferentially transcribed in the metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour calls). AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour calls or issue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for disquosis, prognosis, monitoring and transcripts can be used for disquosis, where metastatic. Diagnosis is compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially or accines; for disgnosing breast cancer and for use in gene or cell-based and isolate populations of educate the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter compounds that produce the polypeptides on be used to expand and isolate populations of educated, and these used for adoptive
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                                                                                                   Claim 1; Page 116; 219pp; English.
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Matches 8; Conservative 0
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Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                                             Metastatic breast tumour cell downregulated transcript tag #3642.
                AAZ84408 standard; DNA; 10 BP.
                                                                                                                                                                                    98US-0089853P.
98US-0089997P.
98US-0090039P.
98US-0090040P.
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                                                  (first entry)
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ROBERTS B L
SHANKARA S.
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19-JUN-1998;
19-JUN-1998;
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                                                  07-APR-2000
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                                 AAZ84408;
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RESULT 146
        AAZ84408,
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98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P.

99WO-US013647.

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Gaps

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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and

Roberts BL, Shankara S;

WPI; 2000-106079/09

treatment of cancer

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WPI; 2000-106079/09
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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour thissue (i.e. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour citisme (i.e. are downergulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antisen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antisense used to expand and isolate populations of educated, antisen-specific immune effecter.
Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                        Claim 1; Page 156; 219pp; English.
                                                                                                                                                 treatment of cancer
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Gарв .. 40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other; Query Match
Best Local Similarity 100.
Matches 8, Conservative immunotherapy

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RESULT 147

AAZ82943 standard; DNA; 10 BP (first entry) 07-APR-2000 AAZ82943;

Metastatic breast tumour cell upregulated transcript tag #2177.

Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Homo sapiens

WO9965928-A2

23-DEC-1999.

18-JUN-1999;

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98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998

GENZYME CORP. ROBERTS B L. SHANKARA S. (GENZ) ((ROBE/) I (SHAN/) 8

that are preferentially transcribed in the metastatic breast tumnour that are preferentially transcribed in the metastatic breast tumnour citisque (i.e. are upregulated in metastatic breast tumnour citisque (i.e. are upregulated in metastatic breast tumnour citisque (i.e. are upregulated in the primary or non-metastatic breast tumnour preferentially transcribed in the primary or non-metastatic breast tumnour citisque (i.e. are downregulated in metastatic breast tumnour cells). These transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially or articularly an artigen-encoding sequence for use in gene or cell-based compositions for diagnosing breast cancer and for raising specific antibodies (b). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter components. Tymphocytes, and these used for adoptive Gaps ö Match 10; Score 8; DB 1; Length 10; Local Similarity 100.0%; Pred. No. 1.2e+02; les 8; Conservative 0; Mismatches 0; Indels Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other; Claim 1; Page 118; 219pp; English. TGGACTCG 10 σ 2 TGGACTCG Query Match g Š

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AAZ84948 standard; DNA; 10 BP RESULT 148 AAZ84948,

07-APR-2000 (first entry) AAZ84948;

Metastatic breast tumour cell downregulated transcript tag #4182.

Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; s8.

Homo sapiens,

WO9965928-A2

23-DEC-1999

99WO-US013647

18-JUN-1999;

98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 19-JUN-1998; .9-JUN-1998 19-JUN-1998

(GENZ) GENZYME CORP. (ROBE/) ROBERTS B L.

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that are preferentially transcribed in the metastatic breast tumour transcripts that are preferentially transcribed in the metastatic breast tumour cells. AAZ83942 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells. Drespessor transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences from vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides can be used to expand cand isolate populations of educated, antigen-specific immune effecter immunotherapy
                                                                                                                                                                                                                                                                                                  to AAZ83941 represent tags corresponding to distinct transcripts
                                                                                                                                               Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                  Claim 1; Page 170; 219pp; English.
                                                  Shankara S;
                                                                                                                                                                                                  treatment of cancer.
                                                                                               WPI; 2000-106079/09
  (SHAN/) SHANKARA S.
                                                     Roberts BL,
                                                                                                                                                                                                                                                                                                  AAZ80767
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Gaps . 40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other; Query Match Best Local Similarity 100. Matches 8; Conservative

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CGCTGGCA 15 8 CGCTGGCA 1 ထ à

AAA14157 standard; DNA; 10 BP. (first entry) (revised) 15-SEP-2003 21-JUL-2000 AAA14157;

Polymorphism detection; over-represented sequence; strand bias; organism identification; genomic mapping; octamer; lagging strand; Escherichia coli 0157:H7; PCR primer; ss. E. coli K-12 lagging strand PCR primer, SEQ ID NO:55.

Escherichia coli K12

WO200017399-A2.

30-MAR-2000.

99WO-US021379. 98US-0101011P. 18-SEP-1998; 17-SEP-1999;

(UYNE-) UNIV NEBRASKA-LINCOLN

Benson AK;

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The invention relates to a novel method for the detection of polymorphisms in a DNA sequence. Test DNA and a second DNA are amplified with at least one palt of primers, and the sequence differences between the amplicons are compared. The primers are based on oligonucleotide sequences that are over-represented in the genome of the relevant corganism, and which are biased to one strand. The method can be used to requences that are over-represented in the genome of the relevant compared with an existing database. Secotype or strain, in which case amplicons are analysed for products, common to all members of the specific for strain or serotype, and the results compared with an existing database. The method can also be used to identify an individual, by comparison of results for a test DNA with an existing database. When applied to differential display analysis, pattern differences in the amplicons are determined, particularly by a cyanisms by species, strain or serotype, and to identify genes based on differential display. The method con identify individuals, to classify or granisms by species, strain or serotype, and to identify genes based on differential display. The method can also be used for genomic mapping, detecting changes in expression patterns, genetic linkage studies, medical display. The method can also be used for genomic mapping, medical display, forensics, and agriculture. The method cuses over-represented sequences to prime amplification. These sequences are faitured to complete Escherichiae call genome. The primers are rationally designed compared to the lagging strand of the E. coli K-12 genome. The primers are rationally designed primers based on over represented octamer sequences biased to the lagging strand of the E. coli K-12 genome. These primers and leading strand or primers based on ver-represented octamer sequences biased to the lagging strand of the E. coli K-12 genome. The sequences biased to the lagging crand of the E. coli M-1414 were used in the examplification of liferentiate and fu
                                                                          Detecting DNA polymorphisms, useful e.g. for identifying organisms by species, strain or serotype, comprises amplification with primers based on over-represented oligonucleotide sequences.
                                                                                                                                                                                               Example; Page 28; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standardise OS field)
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Gaps ; 0 0; Indels Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

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CGCTGGCA 15 N 9 CCCTGGCA

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AAZ48447 standard; DNA; 10 BP. 27-MAR-2000 (first entry) AAZ48447;

Microorganism; virus; polymerase chain reaction; food; cosmetic; clinical diagnostic; molecular beacon; PCR primer; ss. Primer specific for C. jejuni.

Campylobacter jejuni

W09963112-A2

99WO-US010940. 18-MAY-1999;

rng

Romick TL,

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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161.

AH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
                                                                                                                                                                                                                          The present invention describes isolated DNA (I) encoding an allograft inflammatory factor-1 (AIF-1). AIF-1 has immunosuppressive, and antinflammatory and antiarteriosclerotic activities. AIF-1 is an inhibitor of expression of allograft factor such as Gal/GalNAc macrophage lectin. AIF-1 is useful for diagnosing and treating allograft rejection and other conditions associated to vascular inflammation, especially atherosclerosis. The present sequence represents a PCR primer which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynuclectides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular
                                                                                  DNA encoding an allograft inflammatory factor-1, useful for diagnosing and treating allograft rejection and other conditions associated with vascular inflammation, especially atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, transcriptome, gene expression pattern, cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human colon epithelium specific transcriptome sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
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40.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 40; 94pp; English.
                                                                                                                                                                                      Example 1; Col 6; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-2000; 2000WO-US031922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00448480,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH63243 standard; cDNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-367706/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGCTGGC 14
                                           WPI; 2000-430614/37.
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Russell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-2001
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'n,
Utans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 152
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                                                                                                                                                                                                                                                                                                                                                The invention provides a novel in vitro method for the detection of microorganisms and viruses. The method comprises: (1) forming a microorganisms and viruses. The method comprises: (1) forming a predetermined polymerase chain reaction (PCR) mixture by combining a predetermined couprising 5'-TAGAAGC-3', known amounts of a first primer comprising 5'-TAGAAGT-3', and a second primer comprising 5'-AGAAGTTCCCAAAGTCCCAAAGT-3', and a second primer comprising 5'-AGAAGTTCCTAAC-3', and PCR reagents; (2) forming a PCR product by cycling the PCR mixture to amplify the nucleic acid sequence, if present, complicate and attain 0.25-10000mug nucleotide product/mul mixture; (3) adding a probe containing DNA comprising 5'-GTGTGCTACTAAGCCACC-3' to the PCR mixture or to the PCR product to cause the DNA to hybridize with the nucleic acid sequence, if present, and change the conformation of the probe, and (4) determining whether or not bacteria are present in the probe on a sample by detecting the conformational change indicating the presence of bacteria in the sample. The methods can be used for the detection of viruses and microorganisms, the conformational change indicating the presence of bacteria in the sample. The methods can be used for the detection of viruses and microorganisms, the dod and cosmetic industry and in clinical diagnostics. Using the method it is not necessary to remove non-hybridized probe from the system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allograft inflammatory factor 1, AIF-1, AIF-2, allograft gene, screening; diagnosis, allograft rejection; vascular inflammation; atherosclerosis; immunosuppressive, antiinflammatory; antiarteriosclerotic; PCR primer;
                                                                                                                                                                                                                                       for use in the food and cosmetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allograft inflammatory factor related PCR primer SEQ ID NO:28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%; Score 8; DB 1; Length 10; larity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         Detection of microorganisms and viruses, industries and for clinical diagnostics.
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 25; 63pp; English.
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AAA65614 standard; DNA; 10 BP.
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                         98US-0086025P.
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                                                                                               (HUNT-) HUNT WESSON INC
                                                                                                                                                  Fraser MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 TCGCTGGC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGCTGGC 2
                                                                                                                                                                                           WPI; 2000-086985/07.
                         18-MAY-1998;
17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-NOV-2000
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Rattus sp.

AAA65614;

RESULT 151

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Gaps

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Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                       40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:221.
Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                 AAF33482 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2000; 2000WO-US016223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00335032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001 (first entry)
                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae
                                                                                                                                                                                                                                         3 ATGGACTC 10
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                                                                                                                                                                                  1 ATGGACTC 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF33482;
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                       RESULT 153
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                    AAF33482/
XXX
AAF33482/
XXX
AAF33482/
XXX
AAF33-M
XXX
AAF33-M
XXX
AAF33-M
AAF3
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes comprising a SAGE (scrial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having contacting a yeast cell comprising contacting a yeast cell with a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and class of drugs having a characteristic cell with a candidate drug and expression in a yeast cell comprising contacting a yeast cell with a candidate drug and conticuing expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used to identify candidate drugs which affect the cell cycle in methods may be used to identify candidate drugs which affect the cell cycle the cell cycle and for identification of antifungal drugs which affect the cell cycle the cell cycle and for identification of antifungal drugs which affect the cell cycle of antification of antifungal drugs. Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Claim 1; Page 26; 419pp; English.

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represent SAGE tags used in the exemplification of the present invention AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
                                                                               Gaps
                                                                                                                                                                                                                                                   Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE; serial analysis of gene expression; antifungal; tag; identification;
                                                                               ;
                                                                              0; Indels
                                                            Length 10;
                                                                                                                                                                                                                                  Yeast NORF gene SAGE tag oligonuclectide SEQ ID NO:4957.
                                       Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
                                                           DB 1; Ler
                                                           Query Match 40.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Kinzler K;
                                                                                                                                                                        AAF38218 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                                    14-JUN-2000; 2000WO-US016223.
                                                                                                                                                                                                                                                                                                                                                                                                                             Jelculescu V, Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                     linker, PCR primer, ds.
                                                                                                    GCACGCAC 20
                                                                                                                       10 GCACGCAC 3
                                                                                                                                                                                                                                                                                                                            WO200077214-A2.
                                                                                                                                                                                                                                                                                                                                                                                       16-JUN-1999;
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                                                                                                                                                                                            AAF38218;
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                                                                                                                                                      RESULT 154
                                                                                                                                                               AAF38218
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (3) a method (M2) for screening candidate or antifungal drugs comprising; (a) contacting a test substance which modifies the expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA, with a probe which comprises at least 10 comprising contacting unantifying a candidate drug as a member of a class of dentifying a candidate drug as a member of a class of dentifying a candidate drug as a member of a class of dentifying a candidate drug as a member of a class of dentifying a candidate drug and contacting expression in the yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle; the differentially

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

WPI; 2001-061874/07.

Example; Page 177; 419pp; English.

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expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF31268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33267 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
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Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

ö 0: Indels DB 1; Length 10; 1.2e+02; 40.0%; Score 8; DB 1 100.0%; Pred. No. 1.2 iive 0; Mismatches Query Match
Best Local Similarity 100.
Matches 8; Conservative 5 ACTCGCTG 12 ò 셤

m 10 ACTCGCTG AAF40202 standard; DNA; 10

AAF40202;

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(first entry) 23-MAR-2001 Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6941.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

UNJO) UNIV JOHNS HOPKINS

Kinzler K;

Vogelstein B, WPI; 2001-061874/07. Velculescu V,

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 247; 419pp; English

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannocated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression contacting human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contisting contacting human DNA with a probe which comprises at least 10 contisting contacting human paracteristic effect on gene expression in a class of drugs having a characteristic ceffect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and

monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used as markers of phases of the cell cycle. The cycle and for identification of antifungat drugs which affect the cell cycle and for identification of antifungation of the present invention. AAF33268 to AAF33268 to AAF33268 to AAF33268 to AAF33268 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention expression in the yeast cell of at least 1 NORF gene whose 888888888888888

Seguence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

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Gaps

Gaps ô DB 1; Length 10; ., 1.2e+02; ches 0; Indels 40.0%; Score 8; DB 1 100.0%; Pred. No. 1.2 ive 0; Mismatches 40.08; 8; Conservative Query Match Best Local Similarity Matches

. 0

1 ATGGACTC

ò g RESULT 156

AAF37632 standard; DNA; 10 AAF37632

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AAF37632;

(first entry) 23-MAR-2001

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4371.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGB; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

SNING OF THE HOPKINS

Kinzler K; Vogelstein B, Jelculescu V,

WPI; 2001-061874/07.

analysis of Yeast gene coding sequences comprising NORF genes with serial gene expression (SAGE) tags, useful for studying, monitoring a affecting phases of the cell cycle.

Example, Page 156; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) gene comprising a SAGB (serial analygis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human penes which are probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contacting human DNA with a probe which comparises at least 10 contacting human DNA with a probe which comparises at least 10 contacting human DNA with a probe which comparises at least 10 contacting human DNA with a probe which comparises at least 10 contacting contacting human DNA with a probe which comparises at least 10 contacting contacting contacting contacting contacting human DNA with a probe which contacting comprising contacting human DNA with a probe which comprises at least 1 contiguous nucleotides of a NORF gene whose expression varies as in M1;

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and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

0; Indels 40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; ative 0; Mismatches 0; Indels Query Match Best Local Similarity luv... S; Conservative 4 GACTCGCT 11 ઠ dd

1 GACTCGCT 8

AAF37418 standard; DNA; 10 BP RESULT 157

AAF37418;

(first entry) 23-MAR-2001

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4157.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle; NORF, nor previously assigned open reading frame; nonannotated ORF; SAGE, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000,

14-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Kinzler K; Vogelstein B, Velculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 148; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for

comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORR gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a peast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell represent RAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention. genes which are involved in cell cycle progression identifying human

Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

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Gaps

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Gaps . 0 Query Match

40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels

; 0

à d

AAF40866 standard; DNA; 10 BP.

AAF40866;

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonuclectide SEQ ID NO:7605.

Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032. 16-JUN-1999;

SNING ONIV JOHNS HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 271; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M.) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cest 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast RESULT 118

AAP40866/6

XXX

XXX

AAP40

XXX

BAP40

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cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at last 10 contagous mucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a creation of partial mannicoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially corpression used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs. ARF33268 to ARF4064 represent shown the exemplification of the present invention.

ARF33262 to ARF33267 represent inheres and PCR primers used in the SAGE method, in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated UO-44 nucleic acid molecule useful for treating or diagnosing uterine and/or ovarian cancers, comprises sequence corresponding to uterine estrogen agonist-inducible genetic sequence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; oestrogen agonist-inducible; hUO-44; cytostatic; ovary; uterine cancer; ovarian cancer; uterine growth; uterine; development; ovarian growth; ovarian development; oestrogenic activity; PCR primer;
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                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       Sequence 10 BP; 2 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
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(HUGH/) HUGHES E J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH77187 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat arbitrary PCR primer AP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-2001; 2001WO-AU000379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-2000; 2000US-0194566P.
15-AUG-2000; 2000AU-00009471.
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                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGCTGG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP-1; SS.
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 159
AAH77187/C
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The sequence represents the rat arbitrary PCR primer AP-1, used in the invention to amplify cDNA from rat ovary tissue. The invention relates to a novel isolated UO-44 nucleic acid molecule comprising a sequence of

Example 2; Page 37; 82pp; English.

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Gapa

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nucleotides corresponding to a uterine oestrogen agonist-inducible genetic sequence in a mammal. The UO-44 sequences of the invention have vytostatic activity. The UO-44 polynucleotide is useful in the manufacture of a medicament for the treatment of a condition in a mammal, for treating, diagnoshing, detecting or monitoring uterine cancers and/or ovarian cancers, and for producing the polypeptide. The polynucleotide or polypeptide is useful for monitoring uterine and ovarian growth and development and the level of gestrogenic activity in tissue including cancer tissue. They are also useful for the generation of a range of therapeutic molecules capable of modulating oestrogen agonist-mediating cell growth and proliferation in the uterus including ovaries. The UO-44 polypeptide is useful to screen for naturally occurring antibodies to itself
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genotyping protease inhibitor 4 gene of individual for determining haplotype of individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymorphic site; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to genotyping protease inhibitor (PI) 4 (kallistatin) gene of an individual, involves determining for the two copies of the Pid gene present in the individual, the identity of the nucleotide pair at one or more polymorphic sites. PI4 gene is located chromosome 14g31-g32.1. Genotyping is useful for determining if an individual has a haplotype or haplotype pairs defined in the specification. Haplotype or haplotype pairs defined in the relability of several steps in the discovery and development of drugs for treating diseases associated with PI4 activity, e.g. acute pancreatitis, to validate PI4 as a candidate agent for treating a specific condition or disease predicted to be associated with PI4 activity, and in the design of clinical trials of candidate drugs for
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                              DB 1; Length 10; 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, proteage inhibitor, P14; kallistatin, therapy,
PS; haplotyping, genotyping, acute pancreatitis, drug
antiinflammatory, chromosome 14q31-q32.1; primer, 8s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer #28 to detect human PI4 gene polymorphisms.
                                                                                                                                                                                                                                                                                   Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                            , Match
Local Similarity 100.0%; Pred. No. 1.2
tes 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi JY, Koshy B, Sanchis A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD26026 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                    9 TCGCTGGC 2
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                                                                                                                                                                                                                                                                                                                                                                                                               7 TCGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200179227-A2
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                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 160
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Matches
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02-JUL-2002 (first entry)
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ACF12803/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new microsatellite DNA derived from a Pyrus plant and discrimination of Pyrus plants by using it.
treating a specific condition or disease predicted to be associated with PI4 activity. The PI4 gene is useful in studying the expression and function of PI4, and in expressing PI4 protein for use in screening for candidate drugs to treat diseases related to PI4 activity. The present sequence is a primer to detect human PI4 gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a novel microsatellite DNA sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrus plants. The invention also comprises a method for discriminating Pyrus plants - utilising the novel Pyrus microsatellite DNA. The novel microsatellite DNA sequence can be used in discriminating Pyrus plants. The present DNA sequence represents a PCR primer specific for a novel Pyrus pyrifolia (sand pear) microsatellite DNA sequence
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                                                                                                                                                                                                                                                                                           Sand pear, ss; PCR; primer, novel microsatellite DNA sequence; Pyrus plant discrimination.
                                                                                   40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                               Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        Novel sand pear microsatellite DNA PCR primer 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 5; 22pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000JP-00220339
                                                                                                                                                                                                         AAL42350 standard; DNA; 10
                                                                                                                                                                                                                                                  (first entry
                                                                                                          Conservative
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                                                                                                                               9 GCTGGCAC 16
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                                                                                                                                                    GCTGGCAC 3
                                                                                               Local Similarity
hes 8; Conserv
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les 8; Conserv
                                                                                                                                                                                                                                                                                                                             Pyrus pyrifolia
                                                                                                                                                                                                                                                                                                                                                 JP2002034597-A.
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                                                                                                                                                    10
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                                                                                      Query Match
                                                                                                                                                                                             RESULT 162
ABK68734
ID ABK687
XX
AC ABK687
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Matches
                                                                                                                                                                                    RESULT 161
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Matches
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The present invention relates to a new polymucleotide with a sequence comprising an olfactory receptor, family 11, subfamily A, member 1 (CRILAI) isogene selected from 9 isogenes, with regions of a fully defined 8980 base pair sequence given in the specification. The polymorphisms controlled a locations are given in the specification. The invention is useful to haplotyping and genotyping the ORILAI gene in an individual. Other uses include predicting a haplotype pair for ORILAI gene of an individual, and for identifying an association between a trait and at controlled predicting the papers of ORILAI gene. The polymeptide is also useful in studying the expression and function of ORILAI, and in expressing ORILAI protein for use in screening for candidate drugs to creat diseases related to ORILAI activity of ORILAI as well as on the binding affinity of candidate drugs targeting ORILAI for the treatment of olfactory disorders. Without requiring any a prior knowledge of the binding affinity of candidate drugs targeting ORILAI for the treatment of the method of the invention provides the scientist with a tool to confeation of compounds that are more likely to show efficacy in clinical density lead compounds that are more likely to show efficacy in clinical confeation to detect polymorphisms in the human ORILAI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel genetic variants of Olfactory receptor, family 11, subfamily A, member 1 gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. olfactory disorders.
                                 Human; olfactory receptor, family 11, subfamily A, member 1; OR11A1; isogene; haplotyping; genotyping; olfactory disorder; SNP; primer; 88; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Human OR11A1 gene polymorphism detection oligonucleotide primer #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACF12803 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-2001; 2001WO-US027265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-2000; 2000US-0229226P.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kliem SE, Koshy B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GACTCGCT
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                                                                                                                                                                                                                                                                             WO200218657-A1.
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    07-MAR-2002
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The present sequence relates to a new isolated nucleic acid molecule, which is expressed in endometrium and placenta and is upregulated in pregnant uterus and is highly expressed during placental development, encodes a protein having serine protease activity and has an insulin-like growth factor (IGF)-binding motif. The compound is considered gynecological, cytostatic and cardiant. The enzyme is specifically expressed in association with empty implantation and placentation in a pregnant uterus. The mucleic acid is useful for preparing a composition for treating PRSP-related condition e.g., infertility, endometriosis, cancer or a disease of the heart, testis or ovaries. Further, it is useful for detecting, diagnosing or monitoring a condition involving a change in PRSP expression. The sequence is present in the exemplification
            Endometrium, placenta, serine protease, gynecological; cytostatic, cardiant, PRSP, infertility, endometriosis, cancer, pregnancy, primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colorectal cancer; colorectal adenoma; 88; human; renal dipeptidase; macrophage inhibitory cytokine; MIC; RDP; faeces; blood; kidney proximal tubule.
                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding a protein having serine protease activity an insulin-like growth factor-binding motif, useful for preparing a composition for treating a pregnancy-related serum protease-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA tag from human transcript repressed in adenomas/cancers #173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                   (PRIN-) PRINCE HENRY'S INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 55; 156pp; English.
                                                                                                                                                                                  30-JUL-2002; 2002WO-AU001010.
                                                                                                                                                                                                                 30-JUL-2001; 2001AU-0006707
                                                                                                                                                                                                                                                                                                                                                                                                          condition e.g., infertility
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es 8; Conservative
                                                                                                                                                                                                                                                                                      Nie G, Salamonsen LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TCGCTGGC 14
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                                                                                                                WO2003011905-A1.
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                                                                                                                                                 13-FEB-2003
                                                                                Synthetic.
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                                               PCR; ss.
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The invention relates to detecting CC (colorectal cancer e.g. colorectal adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC) cor renal dispetitaise (RDP) in faces or blood of a subject and comparing amount of MIC or RDP in taces or blood of a subject where and comparing amount of MIC or RDP detected to that in normal subjects, where of CC in elevated amount of MIC or RDP in the subject is an indicator of CC in RDP or RDP mRNA in the mRNA sample from facese of a subject, detecting MIC or RDP mRNA in the subject is an indicator of CC in subject; (c) isolating epithelial calls from blood of a subject, isolating an mRNA corrected to that in normal subjects, where an elevated amount of MIC or RDP mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in the mRNA sample to amounts of MIC or RDP mRNA in normal subject, where an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative of CC in the subject; (d) contacting blood or facese of a subject, with a RDP substrate, detecting activity of RDP in the blood or faces by detection of increased reaction product or decreased RDP substrate, and comparing the amount of activity of RDP in the blood or faces of the subject is an indicator of CC in the subject; where an elevated amount of activity of RDP in the blood or faces of the subject is an indicator of CC in the subject in the moiety in the subject from outside of the subject and detecting the moiety in the subject from outside of the subject and care of localisation of the kidney identifies CC; or (f) administering to a subject from outside of the subject, and care of localisation of the kidney identifies of the subject or detecting in the subject is an indicator or RDP in the subject or detecting 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detecting in the faeces or blood RDP reaction product or RDP substrate with the detectable moiety, where increased product or decreased substrate in the faeces or blood indicates CC in the subject. The methods are useful for detecting colorectal cancer in a subject. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is a DNA tag derived from a human transcript whose expression is
                                                                                                                                                                                                                                          Detecting colorectal cancer in a subject, involves detecting macrophage inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood of the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incorrectly called sequence by intensity ratio method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repressed in colorectal cancer or colorectal adenoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                   UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                   Buckhaults P, Kinzler KW, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 31; 59pp; English.
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09-SEP-2002; 2002WO-US028518.
                                            07-SEP-2001; 2001US-0317494P.
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                                                                                                                                                                                                                        MPI; 2003-313220/30.
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Best Local Similarity
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AAX05787
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Findlay JK;

Li Y, Hampton AL,

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Gaps

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40.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels

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(first entry)

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                                                                                                                                                                                                                                                   The invention relates to a computer system for analysing nucleic acid sequences. The computer system is used to perform multiple methods for determining unknown bases by analysing the fluorescence intensities of hybridized nucleic acid probes. The results of individual experiments may be improved by processing nucleic acid sequences together. Comparative analysis of multiple experiments is also provided by displaying reference sequences in one area and sample sequences in another area on a display device. The computer system is also used to identify mutations in a sample nucleic acid. Sequences AAXOS784-787 repersent sequences with
                                                                                                                                                                                                   Identification of unknown base in nucleic acid sequence - using computer system to compare sequences by fluorescent intensities.
                                                                                                                                                                                                                                                                                                                                               mutant bases that were incorrectly called by the intensity ratio method
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wound healing; non-MRL healer mouse; quantitative trait locus; QTL; healing response; microsatellite marker; treatment; central nerve; peripheral nerve; nerve injury; SAGE tag; murine; ss.
Computer system; nucleic acid analysis; fluorescence intensity; hybridized; nucleic acid probe; mutation identification; mutant; intensity ratio; ss.
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                                                                                                                                                              Lipshutz RJ
                                                                                                                                                                                                                                                                                                                                                                  Seguence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                             Bernhart DH,
                                                                                                                                                                                                                                   Disclosure; Page 45; 78pp; English.
                                                                                                                                          (AFFY-) AFFYMAX TECHNOLOGIES NV
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98US-0097937P.
98US-0102051P.
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                                                                                                                                                              Jevona LC,
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                                                                                                                       94US-00327525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                 WPI; 1996-279562/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGCACG 8
                                                                                                                                                               Wang C,
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26-AUG-1998;
28-SEP-1998;
                                                                                                                       21-OCT-1994;
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                                         Unidentified
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                                                                                 19-JUN-1996
                                                             EP717113-A2
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This invention describes a novel non-MRL healer mouse (M) having at least one quantitative trait locus selected from those given in the specification, exhibiting an enhanced healing response to a wound compared to mice (M) without the locus. The invention describes a novel method of identifying a gene involved in enhanced wound healing by identifying a gene involved in enhanced wound healing by described an enhanced wound healing by identifying microsatellite markers which segregate with enhanced wound healing at least one enhanced wound healing gene is chromosomal locus containing at least one enhanced wound healing gene identified. A method a treating a wound in a mammal is also disclosed. The new methods are useful for treating wounds, especially central and peripheral nerve wound. The methods of the invention are useful for restoring function after nerve injury in a mammal. (M) is useful as a mammalian model of enhanced wound healing, useful for identifying genes methods for wound healing. Azisels-Zist represent murine SAGE tags from the method for which are used to illustrate the method of the
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                                                                                                                                 model for enhanced wound healing - useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutation; fluorescent intensity; probe intensity; hybridization; cystic fibrosis; P53 gene; cancer; HIV; genetic characteristic; ss.
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                                                                                                                                                                                                                                                    Claim 13; Page 74; 136pp; English.
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                                                                                                                                                                        enhanced wound healing genes
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                                                                WPI; 1999-494533/41
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Heber-Katz E;
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Disclosure; Fig 20; 59pp; English

The invention provides a method of identifying mutations in sample nucleic acid, by analyzing fluorescent intensities of hybridized mucleic acid probes using a computer system. The method comprises: (a) inputting a first set of probe intensities; ach of the probe intensities is associated with a nucleic acid probe, indicating hybridization affinity between the associated mucleic acid probe intensities, each of the probe intensities is associated with a nucleic acid probe and indicating sequence; (b) inputting a second set of probe intensities is associated with a nucleic acid probe and indicating hybridization affinity between the associated nucleic acid probe and the probe intensities is associated nucleic acid probe and the cample sequences; (c) the computer system comparing probe intensities in the second set to select to select the probe intensities in the second set differ, with each region the probe intensities in the second set differ, with each regions to including multiple base positions; and (d) identifying mutations in the second conding to characteristics of the probes at specific conditing multiple base positions; and (d) identifying mutations in the second conditions, it becomes possible to extract information such as the monomer sequence of bNA, or RNA. Such systems can be used to form e.g. arrays of the probes in the selected regions. The probes is the PSI gene (relevant to certain cannows). HIV, and other conditions is and process the vast amounts of information now used and made available by pioneering technologies

Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

ö Gaps . 0 40.0%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 1.3e+02; ative 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 8; Conservative

10 CTGGCACG 17

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AAF90178 standard; DNA; 11 BP. AAF90178;

(first entry) 06-AUG-2001 used in a computer implemented method.

Mutation; cystic fibrosis; P53 gene; cancer; HIV; protease gene; human immunodeficiency virus; ss.

Synthetic.

US6242180-B1

98US-00158765 23-SEP-1998; 05-JUN-2001

94US-00327525. 95US-00531137. 21-OCT-1994; 16-OCT-1995;

(AFFY-) AFFYMETRIX INC

Chee MS

WPI; 2001-373810/39

Computer implementation for calling unknown bases in a sample nucleic acid sequence involves calling bases according to probe intensities, identifying mutant base call, and analyzing probe intensities near suspected mutation.

Disclosure; Col 49; 59pp; English

The specification describes a computer implemented method of calling unknown bases in a sample nucleic acid sequence. The method comprises calling bases of the sample nucleic acid sequence according to inputted probe intensities, identifying a mutant base call, analysing probe intensities of positions near the suspected mutation, and changing the mutant base call to nonmutant base call if probe intensities are inconsistent of a mutation. The method is used to study and detect mutations relevant to cystic fibrosis, the P53 gene (relevant to certain cancers), human immunodeficiency virus, and other genetic characteristics. The present sequence is used in the course of the invention X00000000000000X8

Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Gaps ; 0 40.0%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 1.36+02; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 8; Conservative Query Match

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10 CTGGCACG 17 ω

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RESULT 169 ABQ87673

ABQ87673 standard; cDNA; 11 BP.

ABQ87673;

10-SEP-2002

Human skin stress/ageing related EST SEQ ID NO 1428.

88 Human; skin ageing; skin stress; EST; expressed sequence tag;

Homo sapiens.

WO200253773-A2.

11-JUL-2002

20-DEC-2001; 2001WO-EP015178.

03-JAN-2001; 2001DE-01000121

(HENK) HENKEL KGAA

Hofmann K; Conradt M, Petersohn D,

WPI; 2002-528865/56.

identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene screening fexpression.

Claim 8; Page 98; 325pp; German.

The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin to identify that genes that show strong differential useful form. (A) comprises protein or mRNAMs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of shin ageing and/or stress; for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention

Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match

Length 11; DB 1; 40.0%; Score 8;

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Human skin stress/ageing related EST SEQ ID NO 851.
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expression.
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Pred. No. 1.3e+02;
: Mismatches 0;
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                                                                                                                                     ABQ86610 standard; cDNA; 11 BP.
 100.08;
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                  8; Conservative
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ABQ86610/c
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ID ABQ87
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AC ABQ87
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The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful. for omprises protein or mRNAMs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; and identifying or determining the effects of sharmaceutical or cosmettic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
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screening for cosmetic or therapeutic agents, based on differential gene
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Human; skin ageing; skin stress; EST; expressed sequence tag;
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nes 8; Conservative
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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmacoutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential expression.
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                                                                                                                                   Claim 8; Page 96; 325pp; German
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or pronoctes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; roacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (ESI) of the invention
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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40.0%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels

ilarity 100.0%; P. Conservative 0;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically schooled from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed and quantify their expression.

(M1) is useful for identifying genes and quantify their expression. determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaals; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell cardinoma; and cardinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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                                                                 Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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 21-OCT-2002 (first entry)
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                                    Human skin EST 115.
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ABV71734/c
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                                                                                                                                                                                                                                                                                       Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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0; Mismatches
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e.g. skin cancer.
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ABV72051/c
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Pred. No. 1.3e+02;
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                                                                                     Hofmann K;
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100.0%; Pre
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                                              The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaas, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BST) of the invention
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Disclosure; Page 83; 1345pp; German.
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ABV68016 standard; cDNA; 11

RESULT 181 ABV68016/c ID ABV680

(first entry)

21-OCT-2002

ABV68016;

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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; soleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; cosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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rosacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of skin. The present seguence is that of a human expressed seguence tag (EST) of the invention
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                                                                                                 h 40.0%; Score 8; DB 1; Length 11; Similarity 100.0%; Pred. No. 1.3e+02; 8; Conservative 0; Mismatches 0; Indels
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                                                                     Sequence 11 BP; 1 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                               Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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skin cancer.

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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immunosuppressive, antiinflammatory, cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin cincholates, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; scoacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

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ABV71370 standard; cDNA; 11
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RESULT 185
ABV71370/c
ID ABV71370/c
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DE Human;
XW Human;
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGB, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens,

NO200253774-A2

11-JUL-2002

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA

Hofmann K; Σ Petersohn D,

WPI; 2002-590638/63

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Claim 24; Page 294; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically scored from skin, to serial analysis of gene expression (\$AGE) so as to identify skin-expressed genes and quantify their expression (\$AGE) (M1) is useful for identifying genes involved in skin homeostasis to determine skin homeostasis and to test agent (M) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis; atopot dermatitis, acne; sebornrea; lupus expressed since for the can be used for the can be used for the can be used for the can as all the described to the can be used for the can get the can be used for the can get the can be used for the can get the described to the can be used to the can be used to the can be used the can be used to the can be use the invention

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ABV68998 standard; cDNA; 11 BP.

RESULT 187 ABV68998 ID ABV689

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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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40.0%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; inchthyosis; atopby dermatitis, acne, seborrhea; lupus expressed sich rosaces, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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                                                                                                             Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                               21-OCT-2002 (first entry)
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                                                                               Human skin EST 6784
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Hofmann K;

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                                                                                                                                                                            In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No.
                                                                                                                                                                                                                                Claim 24; Page 302; 1345pp; German.
                                                                                                                             Hofmann
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95US-00531137.
98US-00158765.
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                                                20-DEC-2001; 2001WO-EP015179.
                                                                        03-JAN-2001; 2001DE-01000127.
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                                                                                                                                                     WPI; 2002-590638/63.
                                                                                                  HENK ) HENKEL KGAA
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                                                                                                                              Petersohn D,
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ABK47234
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Gaps ;

40.0%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels

The invention described a computer system for identifying an unknown base in a sample nucleic acid sequence. The method comprises analysing the fluorescence intensities of nucleic acid probes hybridised with at least one sample nucleic acid sequence. The computer system is useful for visualising, evaluating, and comparing biological sequences, for analysing fluorescent image files of a chip containing hybridised nucleic acid probes to call bases in a sample of nucleic acid sequence, and for identifying an unknown base in a sample nucleic acid sequence. This sequence represents an oligonucleotide used to demonstrate the nucleic Computer aided method of identifying unknown base in sample nucleic acid sequence, comprises analyzing the fluorescence intensities of nucleic acid probes hybridized with at least one sample nucleic acid sequence. Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other; acid analysis system described in the invention Disclosure; Fig 20; 53pp; English

h Similarity 100.0%; Score 8; DB 1; Length 11; Similarity 100.0%; Pred. No. 1.3e+02; 8; Conservative 0; Mismatches 0; Indels 10 CTGGCACG 17 Query Match Best Local Similarity Matches 8; Conserv à

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Gaps

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1 creccace 8

RESULT 190 AAX54872

AAX54872 standard; DNA; 12 BP. AAX54872;

C/EBP-beta antisense oligonucleotide fragment.

(first entry)

05-JUL-1999

Antisense oligonucleotide, multiple target, antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasconstriction; inflammation, allergic rhinitis; acute asthma; allergy, asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis; prostate cancer; ss

Synthetic.

WO9913886-A1

25-MAR-1999

17-SEP-1998; 17-SEP-1997;

97US-0059160P. 98US-00093972. 09-JUN-1998;

(UYEC-) UNIV EAST CAROLINA

Nyce JW;

WPI; 1999-229400/19.

New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction.

Disclosure; Page 67; 120pp; English.

The specification describes antisense oligonucleotides (AAX52869-X55271)

codoning regions of RNAs corresponding to target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codoning regions of RNAs corresponding to target genes, gene initiation condant for juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX5512-74. These multiple target oligonucleotides from sequences AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, caute asthma, allergies, asthma, impeded respiration, allergic rhinitis, coule asthma, allergies, asthma, impeded respiration, respiratory constructive pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary collisease (COPD), and cancers uch as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, paractic metastasses, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer. Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Gaps ö 0; Indels DB 1; Length 12; . 1.3e+02; 40.0%; Score 8; DB 1 100.0%; Pred. No. 1.3 :ive 0; Mismatches Query Match
Best Local Similarity 100...
Best Conservative

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AAX34405 standard; DNA; 12 BP. AAX34405;

25-JUN-1999 (first entry)

Template sequence Seq ID No: 5.

Rolling template, nucleic acid synthesis; polynucleotide polymerase; gene production; primer; ss. CCCCCCCX8X1X6X1X6X1X6X1X6X8X8X8X8X8X8X8X

Synthetic.

WO9914370-A1

25-MAR-1999.

98WO-US019157. 15-SEP-1998;

97US-00929856

15-SEP-1997;

(HIAT/) HIATT A C. (ROSE/) ROSE F D.

Hiatt AC, Rose FD;

WPI; 1999-244045/20.

Producing specific polynucleotides using rolling templates.

Disclosure; Page 25; 109pp; English.

The invention relates to a method for producing polynucleotides having a defined sequence using rolling templates that successively add nucleotides (nts) to a longer primer and the method comprises: (i) incubating, under annealing conditions, a primer and a template that has a 5'-region not complementary to the primer, a 3'-region complementary to the primer, a 3'-region complementary to being shorter than the primer; (ii) reacting the primer with at least one nt in presence of a template-dependent polynucleotide polymerase to

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extend it by at least one nt (complementary to the 5'-region of template) at its 3'-end; (iii) separating the template and the extended primer; and the valeating the cycle of (i)-(iii) as often as needed to synthesize the desired polynucleotide. The method is especially used to produce genes or their segments. The method provides fast, accurate, inexpensive synthesis of RNA or DNA and is more efficient than chemical coupling processes. It has higher specificity and eliminates the need for deprotection. The products can be cloned directly. The method avoids problems of waste disposal and includes an inherent editing effect (failure sequences will not be extended further in subsequent rounds) so that purification of the end product is facilitated. Synthesis may take optimized for a particular host can be prepared
         8X000000000000X8
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Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

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Query Match 40.0%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.38+02; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                               1 ATGGACTC
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Gaps

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AAA34319 standard; DNA; 12 BP. AAA34319; RESULT 192
AAA34319
XXX
AAA34319
DT 28-JUL
XXX
XX
HUMBH,
XW PHORDH,
XW PULLDER
XW CALCEL
XX CALC

Human adenosine receptor related polynucleotide SEQ ID NO:2008. 28-JUL-2000 (first entry)

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorochioate; impaired respiration; inflammation; allergy; allergy; disease; bronchoconstriction; inhibitor; autiinflammatory; antiallergic, attiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens

WO200009525-A2.

24-FEB-2000,

99WO-US017712 03-AUG-1999; 98US-0095212P 03-AUG-1998;

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.

Disclosure, Page 517; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation,

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cffects afflict the lungs of a subject. They can be used for treating cf. schaemic conditions, pulmonary vasoconstriction, allergies, asthma, cimpeded respiration, respiratory distress syndrome, pain, cystic impeded respiration, respiratory distress syndrome, pain, cystic cfibrosis, pulmonary hypertension, emphysema, chronic obstructive conformary disease (CODD), and cancers such as leukamias, lymphomas, carcinomas, and cancers which may metastase to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the conscinctive and prostate cancer. The reduction of the adenosine content of the conscinctive and prostate cancer. The reduction of the adenosine content of the conscinctive and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present the invention, which correspond to SEQ ID NO:1 to 1815, and then the last 185 captences are also called SEQ ID NO:1 to 185, but the sequences differ cfrom the previously named sequences. SEQ ID NO:11 to 1680 (AAA3333 to AAA3392) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention on the match intention of the intention of the present invention.
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Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

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Gaps
                                 ;
0
                               0; Indels
      40.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
         40.0%;
Query Match

Best Local Similarity 100.
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6 crcccrcc 13 Φ 1 CTCGCTGG

Dp

RESULT 193

AAF20441 standard; DNA; 12 BP. AAF20441;

(first entry) 14-MAR-2001 Human C/EBP polynucleotide fragment #2008.

human; airway disorder; bronchoconstriction; lung inflammation; bundan; airway disorder; bronchoconstriction; lung inflammation; bundant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction, asthma, RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss. X A Z L X B X X B

Ното варіелв.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US008020.

06-APR-1999;

EAST CAROLINA. J W. (UYEC-) UNIV (NYCE/) NYCE

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Claim 14; Page 261; 1592pp; English

8 12:32:42 2004

Tue Jun

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (C) immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with cattoring peptide factors and maignancies, such as stimulating and cattoring peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokine, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, confiding proteins, adhesion molecules and their receptors, cytokines and chemokine receptors, adenosine receptors, bradykinin receptors, cronsmitters, defensins, growth factors, vasoactive peptides and creaptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergic fining and/or antisense (CPD), allergic rhinitis (AR), pulmonary conditions, emphysema, chronic obstructive pulmonary disease (CPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAFIB434 to AAFIB434 represent human polynucleotide in the exemplification of the process.
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Gaps . 0; Indels 40.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; live 0; Mismatches 0; Indels Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other; 8; Conservative Local Similarity Query Match Best Loc Matches

6 CTCGCTGG 13 æ ઠ 셤

ABH86538 standard; DNA; 12 BP 22-FEB-2002 ABH86538; RESULT 194

Oligonucleotide primer SEQ ID NO 286531 for detecting SNP TSC0012735.

(first entry)

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

VO200177384-A2

18-OCT-2001

36-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

Berlin K;

WPI; 2001-657177/75

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Set of oligonucleotides, useful for diagnosis and cell typing, adesigned to detect single-nucleotide polymorphisms and cytosine
                                                                                                    methylation status.
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Claim 1; SEQ ID NO 286531; 29pp + Sequence Listing; German

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

Sequence 12 BP; 4 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Gaps ö 0; Indels 40.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 8; Conservative

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13 GCACGCAC 20 1 4 GCACGCAC ઠ 셤 RESULT 195 ABI10644/c ID ABI10644 standard; DNA; 12 BP.

(first entry) 22-FEB-2002 ABI10644;

. 0

Oligonuclectide primer SEQ ID NO 310617 for detecting SNP TSC0024025

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001,

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine designed to detect methylation status.

Claim 1; SEQ ID NO 310617; 29pp + Sequence Listing; German.

acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 This invention describes novel oligonucleotide primers or peptide nucleic

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                          Gape
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                                                                                                                                                             Query Match

80.0%; Score 8; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.38+02;

Matches 8; Conservative 0; Mismatches 0; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formmat from WIPO at this patchiod, but we obtained in electronic format from WIPO at
                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                     Oligonucleotide primer SEQ ID NO 310576 for detecting SNP TSC0024024.
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            ABI10603 standard; DNA; 12 BP.
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40.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels

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Olek A, Piepenbrock C,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Homo sapiens

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at this point/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                         claim 1; SEQ ID NO 286544; 29pp + Sequence Listing; German
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                             WPI; 2001-657177/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                         SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 1.38+02;
ive 0; Mismatches 0; Indels
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Sequence 12 BP; 3 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.

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ABH86551 standard; DNA; 12 BP

RESULT 199

(first entry)

22-FEB-2002

ABH86551;

06-APR-2001; 2001WO-IB000713.

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Sequence 12 BP; 3 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABH99999 and ABI00010-ABI82073 targresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Matches 8; Conservative
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ABI10579 standard; DNA; 12 BP.

(first entry) 22-FBB-2002 ABI10579;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 310552 for detecting SNP TSC0024024.

Homo sapiens

40200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim i, SEQ ID NO 310552; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

GCACGCAC 10

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RESULT 203

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Matches 8; Conservative 0.
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Tue Jun

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                             Oligonucleotide primer SEQ ID NO 286554 for detecting SNP TSC0012735
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 1.3e+02;
0; Mismatches 0; Indels
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                    ABH86561 standard; DNA; 12
                                                                                           (first entry)
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                           22-FEB-2002
                                                                                                                                                                                                                                        sapiens
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                                                                                                                                                                                                                                        Homo
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 targesem the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

methylation status.

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Homo sapiens,

Claim 1; SEQ ID NO 286564; 29pp + Sequence Listing; German.

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Gaps

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40.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; ative 0; Mismatches 0; Indels

Local Similarity 100. nes 8; Conservative

Best Loc Matches

Query Match

Sequence 12 BP; 2 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                       Oligonucleotide primer SEQ ID NO 310612 for detecting SNP TSC0024025
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ABI10639 standard; DNA; 12
                                                                                                                   22-FEB-2002 (first entry)
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13 GCACGCAC 20
                   4 GCACGCAC 11
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13 GCACGCAC 20 GCACGCAC 11

à 임 SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 286564 for detecting SNP TSC0012735

(first entry)

22-FEB-2002 **ABH86571**

ABH86571 standard; DNA; 12 BP

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Seguence 12 BP; 0 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

40.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 8; Conservative 13 GCACGCAC 20 Query Match ઠે

ABH86499 standard; DNA; 12 RESULT 206 ABH86499/c

BP.

ABH86499

Oligonucleotide primer SEQ ID NO 286492 for detecting SNP TSC0012735 (first entry) 22-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

꿌 Berlin Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 286492; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99889, ABF00010-ABF99889 and ABI0010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formm from WFPO at the printed specification, but the wipo.int/pub/published_pct_sequences Sequence 12 BP; 0 A; 3 C; 6 G; 3 T; 0 U; 0 Other; 8X3333333XX

Gaps 6 DB 1; Length 12; . 1.3e+02; 0; Indels 40.0%; Score 8; DB 1 100.0%; Pred. No. 1.3 artive 0; Mismatches Local Similarity 100. Les 8, Conservative Query Match Best Local Si Matches

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ð 쉱 RESULT 207 ABH86509,

ABH86509 standard; DNA; 12

BP.

(first entry) 22-FEB-2002 ABH86509;

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Gaps

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Oligonucleotide primer SEQ ID NO 286502 for detecting SNP TSC0012735.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

40200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Piepenbrock C, olek A,

Ϋ.

WPI; 2001-657177/75

ij. Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 286502; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABB2073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from NIPO at ftp.wipo.int/pub/published_pct_sequences

Seguence 12 BP; 0 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

40.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; Query Match Best Local Similarity

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                     Oligonucleotide primer SEQ ID NO 310586 for detecting SNP TSC0024024.
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22-FEB-2002 (first entry)
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                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 311216 for detecting SNP TSC0024359.
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                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 310586; 29pp + Sequence Listing; German.
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                                              Berlin K;
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ABI10613 standard; DNA; 12 BP.

ABI10613

RESULT 209
ABI10613/C
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AC ABI106
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13 GCACGCAC 20

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11 GCACGCAC 4

methylation status.

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                       designed to detect methylation status.
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                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 1.3
iive 0; Mismatches
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ftp.wipo.int/pub/published_pct_sequences
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ABH86479/c
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Gaps

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ABH86567 standard; DNA; 12 BP

(first entry)

22-FEB-2002

ABH86567;

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RESULT 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                       Gaps
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                             Match 40.0%; Score 8; DB 1; Length 12; Local Similarity 100.0%; Pred. No. 1.3e+02; les 8; Conservative 0; Mismatches 0; Indels
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                                                                                                     Sequence 12 BP; 0 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                           13 GCACGCAC 20
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Matches
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AC ABH80
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DT 22-F7
DX XX
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COC COLLIG
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                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 286560 for detecting SNP TSC0012735.
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Loca 8; Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
peptide nucleic acid, cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                             Set of oligomucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                  German.
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nes 8; Conservative
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                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic diseorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99899 and ABI00010-ABI82073 tapesent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at this pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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-- 0; Indels
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                                  Piepenbrock C,
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(EPIG-) EPIGENOMICS AG
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ABH86486/C
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Gaps

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0; Indels Length 12;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0;

13 GCACGCAC 20

8 GCACGCAC 1

Oligonucleotide primer SEQ ID NO 286469 for detecting SNP TSC0012735.

ABH86476 standard; DNA; 12 BP.

22-FEB-2002 (first entry)

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at first patent did not man will be a printed specification, but fip.wipo.int/pub/published_pct_sequences
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomeclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF0010-ABF99999, ABF00010-ABF99999, ABF00010-ABF99999 ABF00010-ABF99999 and ABF00010-ABF90010 cancer the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 100.
Matches 8; Conservative
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ABI10600/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 286469; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 BP; 0 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 220
ABI10630
ID ABI10630 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                 06-APR-2001; 2001WO-IB000713
                                                                                                                                                                                                                                                                                                                                                   07-APR-2000; 2000DE-01019173
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
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Sequence 12 BP; 0 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

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22-FEB-2002 (first entry)
ABI10630;
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ö This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Oligonucleotide primer SEQ ID NO 310603 for detecting SNP TSC0024025. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine ô Claim 1; SEQ ID NO 310603; 29pp + Sequence Listing; German. 0; Indels DB 1; Length 12; 5. 1.3e+02; Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other; 40.0%; Score 8; DB 1 100.0%; Pred. No. 1.3 :ive 0; Mismatches ftp.wipo.int/pub/published_pct_sequences 꿌 Berlin 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 Query Match Best Local Similarity 100. Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. methylation status WO200177384-A2. Homo sapiens 18-OCT-2001.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an Oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a Polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entitlenamatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypoteasive, cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in antisense gene therapy. The composition may have a cue in a prophylactic or therapeutic respiratory effect of an entitinflammatory stepricial or therapeutic respiratory of alteriors or ceceptor, producing bronchodilation, increasing levels of adenosine or condition. The sequence data for this patent is not represented in the printed or the printed

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

Disclosure; SEQ ID NO 11377; 872pp; English.

ubiquinone.

Aguilar D;

Pabalan J,

Katz E,

Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S;

Miller S,

Nyce JW,

WPI; 2003-229219/22.

23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC

WO200285308-A2

31-OCT-2002

Homo sapiens

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Gabs
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; Pred. No. 1.3e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            CD28 signal transduction pathway; screening assay;
CD-28-regulated nuclear binding protein responsive; ss
                                                                                                                                                                                                                                                               Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                  Human G-CSF gene enhancer region.
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ID AAQ53920 standard; DNA; 11 BP.
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100.0%;
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(first entry)
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Matches 8; Conservative
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XSXXEXEXEXXXXXXX
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Homo sapiens

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Human C/EBP antisense fragment no.1995.

(first entry)

17-0CT-2003

ABZ96135;

ABZ96135 standard; DNA; 12 BP

GCACGCAC 12 13 GCACGCAC 20

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ftp.wipo.int/pub/published_pct_sequences

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Gaps

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12:32:42 2004

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Tue Jun

Weiss A,

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The present invention describes a vector for increasing the copy number of plasmids, comprising a transposable element containing a high copy number origin of replication capable of transposition into a target plasmid. The vector may be prEANS-SacB, pTRANS or pBacTA, PUC2. The vector an be used to facilitate the cloning of large inserts into BAC plasmids, including full-length genes, the isolation of large amounts of BAC plasmids, and the increased expression of BAC genes. They can also be used to generate shuttle vectors without cloning
portion of T. reesei HAC1 protein (see AAB82975) fused to the Escherichia coli maltose-binding protein malE. The invention provides methods for increasing the secretion of a heterologous protein in a cell by inducing an elevated UPR. This can be achieved by modulating the activity of HAC1. PrC2 or IRE1 in the cell. The cell from which the protein is secreted can be any cell having an UPR, such as mammalian cells, insect cells, yeast and filamentous fungi. The protein of interest can be any secreted protein such as a therapeutic protein of interest can be any secreted on l1-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel vector for increasing copy number and gene expression in plasmids, comprises transposable element containing high copy number origin of replication capable of in vitro transposition into target plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               number; cloning; gene expression; pTRANS; pTRANS-SacB;
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                            Length 11;
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                                                                                                                                                                          Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
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Best Local Similarity 81.8%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 2;
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                  The sequence is that of the enhancer region derived from the human G-CSF gene which is responsive to a CD28-regulated nuclear binding protein. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing secretion of heterologous proteins e.g. lipase and cellulase in eukaryotic cells useful in industry to increase production and facilitate purification, by inducing an elevated unfolded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichoderma reesei bipl promoter unfolded protein response element.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infolded protein response; bipl promoter; protein secretion; ss.
                                                                                                                                                                                                                                                     Screening assay for identification of immunosuppressive drugs -ability to inhibit CD28 signal transduction pathway in T-cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11 BP; 4 A; 3 C; 2 G; 2 T; 0 U; 0 Other
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Pred. No. 1.4e+02;
0; Mismatches 2.
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                                                                                                                                                                                                                                                                                                         Disclosure; Page 5; 18pp; English.
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                                                                                                                    92US-00898639
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                   WO9325712-A1
                                                                                      11-JUN-1993;
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                                                     23-DEC-1993
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Human skin stress/ageing related EST SEQ ID NO 324

(first entry)

10-SEP-2002

ABQ86569

BP.

ABQ86569 standard; cDNA; 11

GACTCTCTGTC

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Hofmann

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Conradt

Petersohn D,

(HENK) HENKEL KGAA

WPI; 2002-528865/56.

20-DEC-2001; 2001WO-EP015178 03-JAN-2001; 2001DE-01000121

WO200253773-A2

11-JUL-2002

Ното варіеля

Claim 8; Page 50; 325pp; German.

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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from expression. (A) comprises protein or mRNAs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining the effects of pharmaceutical or cosmetic agents for control of skin ageing the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ85246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene expression.
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immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene expression.
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Human skin stress/ageing related EST SEQ ID NO 1343.

Homo sapiens

(first entry)

10-SEP-2002

ABQ87588

ABQ87588 standard; cDNA; 11 BP.

RESULT 226 ABQ87588

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2 TGGACTCGCTG 12

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Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match
Best Local Similarity 81.0
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Gaps

identification of skin-expressed genes, useful for determining is and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 154; 1345pp; German

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to sarial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin clostofically neurodermatitis; sunburn; psoriaeis, specifically neurodermatitis; sunburn; psoriaeis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

Sequence 11 BP; 3 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Gaps . 39.0%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 1.4e+02; 2; Indels Mismatches .; 0 Conservative Similarity 9; Conserv Query Match Local Best Loc Matches

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072/c ABV67072 standard; cDNA; 11 BP.

21-OCT-2002 (first entry) ABV67072;

Human skin EST 4858.

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic; SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Hofmann K;

Σ̈́

Conradt

Petersohn D,

WPI; 2002-590638/63

Homo sapiens

WO200253774-A2.

11-JUL-2002

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Hofmann K; Σ Conradt WPI; 2002-590638/63. Petersohn D,

Disclosure; Page 159; 1345pp; German.

e.g. skin cancer.

The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or ABV67072//
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ô disorders, specifically neurodermatitis; sunburn; psoriagis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; roscea, melanoma; basal cell cardinoma; and cardinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss. Gaps . 0 Score 7.8; DB 1; Length 11; Pred. No. 1.46+02; 0; Mismatches 2; Indels promotes skin homeostasis or that can be used for disorders, snearfinally and Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other; ; 0 BP 39.0%; ilarity 81.8%; Conservative 0 20-DEC-2001; 2001WO-EP015179 03-JAN-2001; 2001DE-01000127 ABV71082 standard; cDNA; 11 21-OCT-2002 (first entry) 20 CTGGCACGCAC 11 CTGGCAGTCAC Query Match Best Local Similarity Human skin EST 8868. (HENK) HENKEL KGAA WO200253774-A2 Homo sapiens 11-JUL-2002 2 ABV71082; ABV71082 RESULT 8888888 ઠે 셤

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhes; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BST) of the invention In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other; Claim 24; Page 285; 1345pp; German. e.g. skin cancer.

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Score 7.8; DB 1; Length 11; Pred. No. 1.4e+02; 0; Mismatches 2; Indels

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Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (

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ABV63661;

RESULT 230

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (M) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, subburn, psoriasis; scleroderma;
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                                      Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Human skin EST 8153
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81.8%;
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ABV63661 standard; cDNA; 11
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  GCTGGCACGCA 19
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                                      11 GCTGGGAGGCA
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Best Local Similarity
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Hofmann K;

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03-JAN-2001; 2001DE-01000127

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (SAGE) (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin ichthyosis; stopic dermatitis; acnes; sebornhea; lupus expthematosus; inchivosis; atopic dermatitis; acnes; sebornhea; lupus expthematosus; rosacea; melanoma; basal call carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                               In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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                                                                                                                                                                                                                    Disclosure; Page 45; 1345pp; German.
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Matches 9: Conserv
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                                                                                 Petersohn D,
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically scooled factors from skin, to serial analysis of gene expression. (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to teet agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermaitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Disclosure; Page 117; 1345pp; German.
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Query Match
Best Local Similarity 81.00,
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(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; cosecea, melanomi, basal cell carcinoma; and carcinoma or sarcone of the
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                     Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
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81.8%;
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Matches 9; Conservative
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(EST) of the invention
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Best Local Similarity
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis of that can be used for treating skin disorders, specifically neurodermatitis, sunburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis, acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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ABV63730 standard; cDNA; 11 BP.
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Hofmann K;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaals; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Best Local Similarity 81.0
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                Homo sapiens.
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Hofmann K;
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Best Local Similarity 81.0
Conradt M,
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                                  WPI; 2002-590638/63
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Petersohn D,
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Pred. No. 1.4e+02; 0; Mismatches 2;

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81.8%;

Best Local Similarity 81.8 Matches 9; Conservative

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The present invention relates to methods for increasing the secretion of heterologous protein in eukaryotic cells by inducing an elevated unfolded protein response (UPR). The method involves inducing the elevated UPR by increasing the presence of proteins selful for increasing the secretion of heterologous proteins (e.g. lipase, cellulase, carbohydrase) in eukaryotic cells useful in industry to increase protein yields and to facilitate purification. The present DNA sequence is Trichoderma reessi bipl promoter UPR element, bipUPREI which bind HACI-malE protein. (Updated on 29-AUG-2003 to standardise OS field)
so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to that can be used for trating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heterologous protein secretion; unfolded protein response; UPR; lipase; cellulase; carbohydrase; industry; purification; HAC1-malE protein; bipl promoter; bipUPRE1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing secretion of heterologous proteins e.g. lipase and cellulase in eukaryotic cells useful in industry to increase production and facilitate purification, by inducing an elevated unfolded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saloheimo MLA;
                                                                                                                                                                                                                39.0%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 1.4e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trichoderma reesei bipl promoter UPR element, bipUPREI.
                                                                                                                                                                                 Sequence 11 BP; 4 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valkonen MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Fig 16; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                                                                                                                                                                                                                                                                                        AAD24644 standard; DNA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                     Local Similarity 81.8
                                                                                                                                                                                                                                                                                             2 TGGACTCGCTG 12
                                                                                                                                                                                                                                                                                                                              11 recreréere 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEMV ) GENENCOR INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-033728/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2003
07-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD24644;
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 240
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DB 1; Length 11;

39.0%; Score 7.8;

Query Match

Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of an antisense oligonucleotide which can be used for inhibiting growth or replication of herpesviruses. It corresponds to an antisense sequence of a herpesvirus site, pref. in a gene that is essential for synthesising nucleic acids e.g. the immediate early genes or Wmw65. It can be prepd by solid phase triester or phosphor amidite chemistry or by recombinant DNA techniques. It can be used for treating infection by herpesviruses, e.g. herpes simplex type I (HSV-1) and type (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cycomegalovirus (CWV), human herpesvirus growth or replication may indirectly forestall the progression of events from HIV exposure to the clinical manifestation of AIDS. It may also be useful in the detection, diagnosis and manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-Q24044. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New anti:sense oligo:nucleotide(s) for inhibiting HSV - also used for diagnosis and for inhibiting HIV activation by herpes virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                    HSV, treatment, diagnosis, HSV-1, HSV-2, varicella zoster, Epstein-Barr virus, cytomegalovirus, CMV, HIV, AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.0%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 1.5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 BP; 1 A; 1 C; 8 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                        Herpesvirus inhibiting antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 38; 77pp; English.
                                                                                  AAQ24024 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                 91WO-US006646.
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                                                                                                                                                                                                                                                                                                                                                                                                                            (UYMA-) UNIV MARYLAND BALT:
(UYJO) UNIV JOHNS HOPKINS
                                                                                                                                                              (first entry)
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Best Local Similarity 81.0
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Н
                                                                                                                                             (revised)
         GACACGTTGGC
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                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-1990;
                                                                                                                                             25-MAR-2003
21-SEP-1992
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                                                                                                                                                                                                                                                                                                                                     02-APR-1992
                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                 AAQ24024;
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AAT63015
ID AAT630
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coligonucleotides of series 1,AAT63014-21, have specific anti-mRNA sequences to the 5' untranslated cap region of tumour necrosis factor (TNF) -alpha mRNA. These oligonucleotides are an example of a new chimeric oligonucleotide library, used to identify an antisense binding site in a target mRNA (in this case TNF-alpha). The library comprises a set of distinct chimeric oligonucleotides capable of hybridising to mRNA to form a duplex, the nucleotides sequences of which each have a common length of 7-20 bases. All of the nucleotides of the common length which are present as subsequences in the target mRNA are present in the library. Bach as subsequences in the target mRNA are present in the library. Bach as uncleotides sequence comprises a recognition region recognisable by a duplex-cutting RNAse, and a flanking region of chemically modified nucleotides which binds to the mRNA sufficiently tightly to stabilise the duplex for the RNAse. Each oligonucleotide is protected against chimal effective antisense compounds against specific mRNA targets. The antisense compounds against specific mRNA targets. The antisense compounds against specific mRNA targets. The consideration of the repentic agents, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
                                                                                                                               Tumour necrosis factor alpha; TNF-alpha; therapeutic agent; chimeric oligonucleotide library; antisense binding site; antisense compound; drug target validation; 5' untranslated cap region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric oligo:nucleotide library - for use in identifying anti-sense binding sites in target messenger RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                           INF-alpha mRNA series 1 (5' untranslated cap region) oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 3 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 27; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tools for drug target validation
                                                                                                                                                                                                                                                                                                                                             96WO-GB002275
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AAV32266 standard; DNA; 12
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                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 GCTGGCACGCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-202228/18
                                                                                                                                                                                                                                                                                                                                             13-SEP-1996;
                                                                                                                                                                                                                                                                 WO9710332-A2
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                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1995;
                                                        02-FEB-1998
                                                                                                                                                                                                                                                                                                       20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmidt G;
                                                                                                                                                                                                                              Synthetic
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                    AAT63015
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Matches
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The invention provides a method for the differential screening of gene expression by random primed reverse transcription PCR (RT-PCR). The primer sequences are generated by stimulating PCR reactions on nonrequired mammalian nuclectide sequence databank entries containing at least 1,000 bp of coding region. The primers selected, such as the present one, had to meet various criterial such as having an efficiency index between 2-10, having a selectivity index higher than 1, being 12 bp in at least 5 of the 8 bases at the 3'-end. The invention claims the selected primers make it possible to use internally primed, PCR-based RNA fingerprinting for simple, exhaustive and systematic analysis of differential gene expression as an advantageous alternative to differential display. The method can also be useful for isolating new coding sequences and to compare known and new genes
                                                                                                                                                                                                                                                                                          Differential screening of gene expression by reverse transcription polymerase chain reaction – uses random priming with primers selected for high efficiency and selectivity by computer screening of database(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amplification, polymerase chain reaction, PCR; microorganism, compost, detection, pollutant, soil, food, agricultural chemical, polymer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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39.0%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                           (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
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differential gene expression; ss
                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 24; 37pp; English
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                                                                                                                              97WO-EP005290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GGACTCGCTGG 13
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                                                                                                                                                                                                                              Fesce R;
                                                                                                                                                                                                                                                              WPI; 1998-230725/20.
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                                                             WO9813521-A1.
                                                                                                                              26-SEP-1997;
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21-JAN-2000
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                                                                                                                                                                                                                              Consalez G,
                                                                                              32-APR-1998
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                               Synthetic.
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AAZ41820
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AAA55919
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                                                                                                                                                                                                                                               This invention describes a novel method for the amplification of DNA comprising (i) preparing many primers (P) with different probabilities of many different and (ii) simultaneous polymerase chain reaction (PCR) of many different and the second of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbe detection in organic waste arbitrarily primed PCR primer #181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amplification of a DNA fragment - in order to establish the state of existence of a microbe.
                                                                                                                                                                Novel polymerase chain reaction method, for differentiating between microorganisms and for detecting contaminants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7.8; DB 1; Length 12;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 12 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
                                              (SAOL ) SANYO ELECTRIC CO LTD.
(NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAOL ) SANYO ELECTRIC CO LTD.
(NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 10; 40pp; Japanese.
                                                                                                                                                                                                                        German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ41604 standard; DNA; 12 BP.
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   98JP-00087651.
99JP-00069694.
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                                                                                                                                                                                                                    Example 1; Page 22; 78pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ACTCGCTGGCA 15
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                                                                                                                                  WPI; 1999-592157/51
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Best Local Similarity
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   31-MAR-1998;
16-MAR-1999;
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                                                                                                    Inoue T;
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The present invention describes a method for detecting (D) at least 1 protein-protein interaction (PPI) by recombinantly expressing within a population of fast calls, populations of first and second fusion proteins comprising DNA binding domain (DBD) and transcriptional regulatory domain (TRD) respectively and detecting the regulation of transcription of the nucleotide sequence of host cells operably linked to a promoter driven DBD. The detection method (D) is useful for identifying inhibitors of PDI for therapeutic use, and for detecting specific cell types, tissue types, argae of development and disease states. From the population of the proteins characteristic of the particular tissue or a cell-type, all possible detectable PDI that occur can be identified and genes encoding these proteins can be isolated. Thus, parallel analysis of two cell types enumerates PDI that are common to both and those that are specific to both. This analysis has significant value since PPI specific to a disease
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A method has been developed for the amplification of a DNA fragment in which amplification is carried out on the DNA fragments of a number of different DNAs. The method comprises a PCR reaction repeatedly carrying out a heat-denaturing step, a primer annealing step and a polymerase extending step, to amplify the DNA fragments of a plural of different DNAs. The method can detect the existence of a microbe in organic waste. AAZ41424 to AAZ41639 represent PCR primers used in random amplified polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast; detection; protein-protein interaction; DNA-binding domain; characterisation; identification; protein pathway information; protein interaction domain; screening; PCR primer; adapter; linker; fusion protein; inhibitor; regulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rothberg JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.8%; Pred. No. 1.56+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adapter linker nucleotide sequence SEQ ID NO:78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example, Col 131; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-00874825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAASS919 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 ACTCGCTGGCA 15
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                                                                                                                                                                                                                                                                                                                                      organic waste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-1997;
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Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

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Gaps

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The present invention describes a method for detecting (D) at least 1 protein-protein interaction (PII) by recombinantly expressing within a protein-protein interaction (PII) by recombinantly expressing within a comprising DNA binding domain (DBD) and transcriptional regulatory domain (TRD) respectively and detecting the regulation of transcription of mucleotide sequence of host calls operably linked to a promoter driven by DBD. The detection method (D) is useful for identifying inhibitors of PPI for therapeutic use, and for detecting specific cell types, tissue types, stage of development and disease states. From the population of the proteins characteristic of the particular tissue or a cell-type, all possible detectable PPI that occur can be identified and genes encoding these proteins can be isolated. Thus, parallel analysis of two cell types out. This analysis has significant value since PPI specific to a disease that can serve as therapeutic points of intervention. Inhibitors of PPI can also be isolated in rapid fashion. The number of false positives and low throughput are reduced, AAA55863 and AAA55961 are sequences used in the exemplification of the present invention
can also be isolated in rapid fashion. The number of false positives and low throughput are reduced. AAA55843 to AAA55963 and AAY90961 are sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying, comparing and detecting inhibitors of protein-protein interactions within population of host cells, involves detecting regulation of transcription of nucleic acid sequence by fusion protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast, detection, protein-protein interaction, DNA-binding domain, characterisation; identification, protein pathway information, protein interaction domain; screening; PCR primer; adapter; linker; fusion protein; inhibitor; regulation; ss.
                                                                                                                                  39.0%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 1.5e+02; Conservative 0; Mismatches 2; Indels
                                                                                              Seguence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adapter linker nucleotide sequence SEQ ID NO:79.
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                                                                                                                                                                                                                                                                                                                                                 AAA55920 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                              12
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                                                                                                                                                                                                                TGGACTCGCTG
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                                                                                                                                                       Local Similarity
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                                                                                                                                      Query Match
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Matches
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Rothberg JM;

Nandabalan K,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding mammalian Lhx3 for identifying a human with a disease, disorder, or condition caused by an altered level of expression or binding of Lhx3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated nucleic acid (I) encoding a mammalian Lhx3. (I) is used in assays to: (1) detect and quantify the presence and level of expression of Lhx3. Lhx3a or Lhx3b, in a sample; (2) identify a compound that affects expression, the level of expression, or the activity of Lhx3, Lhx3a, or Lhx3b in a cell; (3) identify a compound that affects expression, the level of expression, of a pituitary trophic hormone gene promoter; (4) identify a human afflicted with a disease, disorder, or condition caused by altered expression of Lhx3 or altered level of binding of Lhx3 to a nucleic acid; and (5) detect a mutation in a Lhx3 allele in a human. The coding region of human Lhx3 has been genomically mapped to the subtelomeric region of chromosome 9. Lhx3 is also known as P-LIM or LIM-3. The present sequence represents a human Lhx3 expression boundary oligonucleotide, which is
                                               Gaps
                                                                                                                                                                                                                                                                                                                             Lhx3, LIM-3, P-LIM; identification; characterisation; diagnosis; chromosome 9; pituitary disease; subtelomeric region; mutation; pituitary trophic hormone gene promoter; ds.
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               Length 12;
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), Sloop KW;
                                             Indels
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                                                                                                                                                                                                                                                                                               Human Lhx3 exon-intron boundary oligonucleotide #4.
            Score 7.8; DB 1; L
Pred. No. 1.5e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 165; 239pp; English.
                                                                                                                                                                                                AAA92134 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2000; 2000WO-US004424.
              39.0%;
81.8%;
                                                                                                                                                                                                                                                                (first entry)
                                               Conservative
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                                                                              2 TGGACTCGCTG 12
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                                                                                                                TGCAGTCGCTG
Query Match
Best Local Similarity
Lag 9; Conserva
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Best Local Similarity
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Showalter AD,
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                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                AAA92134;
                                                                                                                                                                 RESULT 248
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US6083693-A

AAA73431 standard; DNA; 12 BP

(first entry)

09-FEB-2001

AAA73431;

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to reporter
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                                                                                                                                                                                                                                                                          Detecting protein-protein interactions in protein populations useful identifying genes encoding the proteins, and inhibitors of the interactions, by detecting transcriptional regulation leading to repos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7.8; DB 1; Length 12;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amplification of a DNA fragment and its apparatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
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(NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
                                                                                                                                                                                                                                                                                                                                                                              sxample; Col 103-104; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer; amplification; selective; ss.
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81.8%;
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Best Local Similarity 81.8-
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                                                                                                                                                                                                       Nandabalan K, Rothberg
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                                                                                                                                                                  (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                          gene activation.
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                                                                                                                              .4-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting protein-protein interactions in protein populations useful for identifying genes encoding the proteins, and inhibitors of the interactions, by detecting transcriptional regulation leading to reporter gene activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to methods for detecting and isolating genes encoding proteins that interact with each other, via the acconstitution of a transcription factor and hence reporter gene activation. Proteins are fused to either the yeast DNA-binding domain of a transcriptional activator or to the activation domain of a transcriptional activator. The present sequence is a linker used in the present invention as an adapter in the analysis of yeast fusion genes. The present method may be used to identify protein-protein interactions and genes encoding the interacting proteins relevant to a particular tissue, stage or disease e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linker; yeast; two-hybrid system; protein-protein interaction; cancer;
                                                                                                                                                                                                           Linker; yeast; two-hybrid system; protein-protein interaction; cancer;
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Example, Col 103-104; 135pp; English.

96US-00663824 96US-00663824

14-JUN-1996; 14-JUN-1996;

Saccharomyces cerevisiae

US6083693-A

Nandabalan K, Rothberg JM;

WPI; 2000-464335/40.

(CURA-) CURAGEN CORP.

Seguence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match
Best Local Similarity 81.5
Best Local Sy Conservative

2 TGGACTCGCTG 12 rccacrccrc 11

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AAA73432 standard; DNA;

09-FEB-2001

AAA73432;

Linker RC15

Saccharomyces cerevisiae

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This invention relates to a method for amplifying a DNA fragment. The method comprises successive repetitions of heat-denaturing, annealing of a primer and an extending step using a DNA polymerase. The method makes use of a cDNA pool in which the primer is one primer or a pair of primer sets and has an amplification probability which allows it to amplify a DNA fragment from a limited number of the cDNAs among the DNA pool (where the limited number is in the range of 1 to 25). Also included in the invention are apparatus used for carrying out the method, a primer and a bux polymerase and a kit used for amplifying a DNA fragment. The method can be used to amplify a limited number of CDNAs from a pool in which wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acids containing a modified base, especially a substituted vinyl group at the 5-position of a pyrimidine, such that nucleic acids can be reversibly ligated to each other by light-irradiation. The nucleic acids with unique structures can be synthesised for use in gene therapy, DNA computing and immobilisation of nucleic acids. The ligation and immobilisation processes involve the use of light, which is environmentally friendly. The present sequence is that of an oligonucleotide useful to the invention
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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Example 1; Page 11; 32pp; Japanese
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05-JAN-2001; 2001JP-0000750.
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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Sequence 12 BP; 4 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

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Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
Length 12;
Score 7.8; DB 1; Length 12
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                      AAH79164 standard; DNA; 12 BP.
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05-JAN-2001; 2001JP-00000750
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  39.0%;
81.8%;
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Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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                                                        6 CTCGCTGGCAC 16
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                                                                                                                                                                                                                                      Oligonucleotide ODN
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microarray

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The present sequence is a probe used to demonstrate array-based nucleic acid hybridisation. This was an example in a specification relating to a method for producing an array of discrete bloaties comprising non-covalently attached nucleic acids. The nucleic acids are useful as probes in hybridisation reactions. The affinity and selectivity of the non-covalently immobilised probe to sample target duplex formation is excellent and compact compared to conventional methods and unlabelled probes are applied at a concentration which is at least five times lower than required for conventional methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Association device for nucleic acid-based diagnostic test, isolation of nucleic acids, comprises oligonucleotide probe and solid substrate having support surface comprising association surface for linking probe to substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an association/hybridisation device comprising nucleic acid and polypeptide probes, or combinations of these, linked to a porous solid substrate, comprising an external substrate surface and several internal pores. The pore surfaces comprise an association surface which is charged with net positive or negative charge density where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation device, single base pair difference, diagnostic test, protein purification, nucleic acid purification, secondary structure, probe, 88; k-ras; codon 12.
                                                         Producing nucleic acid array for use in hybridization reactions, by employing adsorptive, non-covalent attachment of nucleic acids and oligonuclectide probes to positively charged solid surfaces.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
Local Similarity 81.8%; Pred. No. 1.5e+02;
es 9; Conservative 0; Mismatches 2; Indels
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10-AUG-2000; 2000US-00636268.
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                    WPI; 2001-147356/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA165968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a probe used to demonstrate array-based nucleic acid hybridisation. This was an example in a specification relating to a method for producing an array of discrete biosites comprising non-covalently attached nucleic acids. The nucleic acids are useful as probes in hybridisation reactions. The affinity and selectivity of the non-covalently immobilised probe to sample target duplex formation is excellent and compact compared to conventional methods and unlabelled probes are applied at a concentration which is at least five times lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Producing nucleic acid array for use in hybridization reactions, by employing adsorptive, non-covalent attachment of nucleic acids and oligonuclectide probes to positively charged solid surfaces.
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               d nucleic acid hybridisation; hybridisation probe; capture probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7.8; DB 1; Length 12;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                than required for conventional methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 29; 46pp; English
                                                                                                                                                                                                                                                                                             (GENO-) GENOMETRIX GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENOMICS INC
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray capture probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microarray capture probe k3.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                        Belosludtsev Y;
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                                                                           Unidentified
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                  Array-based
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9

Matches

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AAF56187

IID AAF56187

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XX

I9-7

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XX

Micro

RESULT 255

Belosludtsev IY;

0

Gaps

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8 12:32:42 2004

Tue Jun

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uncleic acid or a polypeptide probe. The device is also useful for associating a mucleic acid or a polypeptide in a sample to a nucleic acid or a polypeptide probe. The device is also useful for a cutecting a single base pair difference between a mucleic acid in a test sample and an oligomuclectide probe. The device finds application in nucleic acids based diagnostic tests, isolation and purification of nucleic acids or polypeptides from a sample. The device can be used at any temperature and the kinetics of association between the oligomuclectide probe and the nucleic acid in the test sample are 10 fold more rapid than the kinetics of association under conditions when the substrate surface or association surface has a neutral or net negative charge density. The device and the method can be used for hybridisation or present sequence is that of a k-ras capture probe. As a representative probes to target DNA or RNA at low bulk ion concentrations. The present sequence is that of a k-ras capture probe. As a representative was used to examine hybridisation rate enhancement under low ionic strength and low ph conditions. The capture probes (AAISS966-AAISS972) comprise biologically significant codon 12 point mutations
   pH is lower or higher than the pI of association surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
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39.0%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 1.5e+02;

0; Mismatches Query Match
Best Local Similarity 81.8
Matches 9; Conservative 4 GACTCGCTGGC 14 1 GACTTGGTGGC 11 ò

RESULT 257 AAI 6597

AAI65971 standard; DNA; 12

(first entry) .5-JAN-2002

Synthetic k-ras codon 12 point mutant capture probe K6.

Hybridisation device; single base pair difference; diagnostic test; protein purification; nucleic acid purification; secondary structure; probe; ss; k-ras; codon 12

Synthetic.

WO200166687-A1.

13-SEP-2001,

24-AUG-2000; 2000WO-US023438.

09-MAR-2000; 2000US-00522240. 10-AUG-2000; 2000US-00636268.

(GENO-) GENOMETRIX GENOMIX INC

Belosludtsev YY, Iverson B, Powdrill T, Hogan M,

WPI; 2001-611328/70.

Belosludtsev IY;

Association device for nucleic acid-based diagnostic test, isolation of nucleic acids, comprises oligonucleotide probe and solid substrate having support surface comprising association surface for linking probe to

Example 13; Page 63; 101pp; English.

The invention relates to an association/hybridisation device comprising nucleic acid and polypeptide probes, or combinations of these, linked to a porous solid substrate, comprising an external substrate surface and several internal pores. The pore surfaces comprise an association surface which is charged with net positive or negative charge density where the

the second that the professoriation surface. The device is useful for associating a nucleic acid or a polypeptide in a sample to a nucleic acid or a polypeptide probe. The device is also useful for detecting a single base pair difference between a nucleic acid in a test sample and an oligonucleotide probe. The device finds application in cucleic acid-based diagnostic tests, isolation and purification of mucleic acid-based diagnostic tests, isolation and purification of any temperature and the kinetics of association between the colliqued probe and the nucleic acid in the test sample are 10 fold concertage than the kinetics of association under conditions when the substrate surface and the mucleic acid in the test sample are 10 fold concertage surface or association surface has a neutral or net negative charge density. The device and the method can be used for hybridisation of probes to target DNA or RNA at low bulk ion concentrations. The present sequence is that of a k-ras capture probe. As a representative present sequence is that of a k-ras capture probe. As a representative consented to examine hybridisation rate enhancement under low ionic strength and low pH conditions. The capture probes (AAI66966-AAI66972) comprise biologically significant codon 12 point mutations

Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

. 0 Score 7.8; DB 1; Length 12; Pred. No. 1.5e+02; 0; Mismatches 2; Indels Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative

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Gaps

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Gaps

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2; Indels

RESULT 258 ABH83492

ABH83492 standard; DNA; 12 BP.

ABH83492;

(first entry)

22-FEB-2002

Oligonucleotide primer SEQ ID NO 283485 for detecting SNP TSC0011339.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1, SEQ ID NO 283485, 29pp + Sequence Listing, German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nuclectide polymorphisms (SMP) and cytosine methylation status in chemically pretreated genomic DMA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010

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ABH85734
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at flow bublished_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                     Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
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81.8%;
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Best Local Similarity 81.0
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Best Local Similarity 81.8
Matches 9; Conservative
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AZESULT 22-FEB
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AZESULT 259
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gestrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC90989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 310591 for detecting SNP TSC0024024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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   DNA;
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ABI10618 standard;
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2 TGGACTCGCTG 12

07-APR-2000; 2000DE-01019173

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC001013 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire, wipo.int/pub/published_pot_sequences
              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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Similarity 81.8%; Pred. No. 1.5e+02;
9; Conservative 0; Mismatches 2; Indels
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Best Local Similarity
                                                                                                                    WO200177384-A2
                                                                                     Homo sapiens
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Berlin K;

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lar; primer; 88;
immune; metabolic.
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39.0%; Score 7.8; DB 1; Lengtl 12;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Inde s
                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and methylation status.
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                                                                                                                                                                                      Claim 1; SEQ ID NO 286512; 29pp + Sequence Listing; Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 290180 for detecting
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                                                            Berlin K;
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                                                            Piepenbrock C,
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                              (EPIG-) EPIGENOMICS AG.
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                                                                                         WPI; 2001-657177/75
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                                                            Olek A,
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06-APR-2001; 2001WO-IB000713,

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Sequence 12 BP; 1 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

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RESULT 266
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               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 targresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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81.8%;
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Best Local Similarity
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ABH94011
AC ABH940
XX ABH940
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XX ABH940
XX SNP; B
KW PEPLIG
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XX CO TAPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovas ular; primer; ss; central nervous system; gastrointestinal; respiratory immune; metabolic.
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Score 7.8; DB 1; I Pred. No. 1.5e+02; O; Mismatches 2;
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   Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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AB123556/C
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AB123556/C
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide; jlymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic diseonders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH0010-ABE99989 and AH:00010-ABE82073 data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascalar; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 274980; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.0%; Score 7.8; DB 1; Lengtl. 12; Best Local Similarity 81.8%; Pred. No. 1.5e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12 BP; 4 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABH86581 standard; DNA; 12 BP
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                                                                                                                              06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                        07-APR-2000; 2000DE-01019173
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                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TCGCTGGCACG 17
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                                       40200177384-A2.
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  Homo sapiens
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                                                                                    18-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 268
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, artdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                 Oligonuclectide primer SEQ ID NO 378891 for detecting SNP TSC0062977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                  ABI78918 standard; DNA; 12 BP
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                                                                                                       (first entry)
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Best Local Similarity 81.0
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TGGACTCGCTG 12
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                                                                                                                                                                                                                                                                                       Homo sapiens.
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AB178918

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AB18

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AB19

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Gaps

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Berlin K;

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS AG.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

RESULT 267

ठ 8 ABH74993

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Gaps

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WPI; 2001-273428/28.
                                            Local Similarity
                                                                                      WO200120026-A2
                                                                                                 10-SEP-1999;
                                                                                                        Wojnowski L,
                                                                                  Homo sapiens
                                                                      29-AUG-2001
                                                                                         22-MAR-2001
                                                                  AAS02759
                                              Matches
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Recombinant adeno-associated virus containing growth cormone gene or related genes, useful for accelerating swine growth and increasing lean meat ratio.
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substrates, inhibitors or modulators of the hPXR gene product. The proteins can be used to identify and obtain prodrugs and drugs for treatment of diseases which are amenable to chemother py. The nucleic acids can be used in gene therapy for the treatment of prevention of disorders associated with hPXR expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV; adeno-associated virus; growth hormone gene; growth, GH; vector; inverted terminal repeat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV containing growth hormone gene related inverted terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.8; DB 1; Length 12;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                         Match
Local Similarity 81.8%; Pred. No. 1.5e+02;
Loc 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                      Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 6; 26pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                      5 ACTCGCTGGCA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175134-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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Matches
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Matches
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                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding sequences and PCR primers of the invention. The human pregnane X receptor sequences are used to make antibodies, or a substance capable of binding specifically to the gene product of hPXR gene, for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel variant of the human pregnane X receptor gene, associated with insufficient metabolization and/or sensitivity to drugs, is useful for diagnosing and treating diseases with drugs that are modulators of their gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                        German
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Pred. No. 1.5e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human pregnane X receptor (hPXR) gene, PCR primer #29.
                                                                                                                                                                        Claim 1; SEQ ID NO 286574; 29pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 1 A; 6 C; 5 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Page 39; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.0%;
81.8%;
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                                     WPI; 2001-657177/75.
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Gaps

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RESULT 271 ABL91654/c

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SpeI 5' PCR primer tail used in Chlamydia pneumoniae gene amplification.
                                                               Chlamydia pneumoniae; chlamydial infection; antigen; immunogen; vacc diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; calaudication; stroke; strain CWLO29; open reading frame, ORF; Escherichia coli; recombinant expression; primer tail sequence; PCR;
                                                                                                                                                                                                                                                                                                                                                                         Example; Page 33; 364pp; English
standard; DNA; 12 BP
                                                                                                                                                                                                              2000GB-00017047.
2000GB-00017983.
2000GB-00020440.
2000GB-0002583.
2000GB-0002549.
                                                                                                                                                                                       03-JUL-2001; 2001WO-IB001445
                                (first entry)
                                                                                                                                                                                                                                                                                                                     WPI; 2002-154726/20
                                                                                                                                                                                                                                                                                   (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                     Grandi G;
                                                                                                                                                     WO200202606-A2
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10-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                         21-JUL-2000;
07-AUG-2000;
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                                 29-JUL-2002
                                                                                                                                                                     10-JAN-2002
                                                                                                                    primer; ss
                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                     Ratti G,
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Kalbileisch TS;

Knight JR,

Yang M,

Nandabalan K, Rothberg JM,

WPI; 2002-654433/70.

(CURA-) CURAGEN CORP.

14-JUN-1996;

13-JUN-1997;

99US-00461125 96US-00663824.

14-DEC-1999;

RC15 linker DNA used to illustrate the method of the invention.

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AAD45523 standard; DNA; 12

11 CTAGTACGCAC 1

27-DEC-2002 (first entry)

AAD45523;

immunogen; vaccine;

Protein-protein interaction; detection; cancer; linker; ss.

Unidentified

US6410239-B1

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Detection of protein to protein interactions amongst two protein populations useful e.g. to identify interactions specific for particular tissues or diseases and to identify inhibitors of interactions uses a new genetic method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are preddicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as theresclerosis, coronary artery disease, carotic artery stenosis, coronary artery disease, acrtic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the proteins and nucleic acids of the invention prevention or treatment of chlamydial infections, particularly Chlamydia prevention or treatment of chlamydial infections particularly chlamydia by proteins and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia DNA probe assay or blotting techniques for determining Chlamydia preventions in the amplification of the novel Chlamydia pneumoniae commander amplification of the novel Chlamydia pneumoniae commander amplification of the novel Chlamydia pneumoniae commander amplification of the novel Chlamydia preumoniae commander amplification of the novel Chlamydia pneumoniae commander amplification of commander amplification of commander amplification of commander amplification of commander am
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Matches 9; Conserv
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39.0%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 1.5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                         AAD45522 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                          (first entry)
                                   Conservative
                                                                    TGGACTCGCTG 12
                                                                                                    recaercecre 11
 Ouery Match
Best Local Similarity
Matches 9, Conserv
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Query Match

10 CIGGCACGCAC 20

06-FEB-2002; 2002WO-US003423

Tue Jun

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The present invention relates to novel methods for detecting protein to protein interactions amongst two populations of proteins, each having a complexity of at least 100. The method involves using new genetic methods in which encoded proteins are fused to either the DNA-binding domain of a transcriptional activator or the activation domain of a transcriptional activator or the activation domain of a transcriptional activator. The methods are useful to detect interacting proteins and to identify protein-protein interactions specific for a particular species, tissue, stage of development or disease state, e.g. by comparing protein protein interactions between populations from cDNA of cancerous or precancerous cells with those from non-cancerous cells. They are also useful to identify inhibitors interfering with protein-protein interactions e.g. potential drug candidates inhibiting interactions specific to cancerous cells. The present sequence is a linker DNA used to illustrate the method
                                                                                                                                                                                                                                                                                                                                                       Detection of protein to protein interactions amongst two protein populations useful e.g. to identify interactions specific for particular tissues or diseases and to identify inhibitors of interactions uses a new genetic method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphoramidite, INVADER assay cleavage reaction, FEN1, cleavase, nucleic acid separation; DNA polymerase, human, MCP-1, ubiquitin, monocyte chemoattractant protein-1; PCR; primer; probe, ss.
                                                                                                                                                                                                                                                                                          Yang M, Knight JR, Kalbfleisch TS;
RC14 linker DNA used to illustrate the method of the invention.
                                 Protein-protein interaction; detection; cancer; linker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7.8; DB 1; Length 12;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Col 197; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS68785 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.0%;
81.8%;
                                                                                                                                                                                                       96US-00663824
97US-00874825
                                                                                                                                                                      99US-00461125
                                                                                                                                                                                                                                                                                            Nandabalan K, Rothberg JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention
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                                                                  Unidentified
                                                                                                     US6410239-B1
                                                                                                                                                                        .4-DEC-1999;
                                                                                                                                                                                                       14-JUN-1996;
                                                                                                                                    25-JUN-2002.
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                                                                                                                                                                                                                                                                   The invention relates to a composition computising a positively or separation feated phosphoramidite. The composition is useful for separation of mucleic acid molecules. The composition is further useful for fractionation of specific nucleic acids by select we charge reversal useful in e.g. INVADER assay cleavage reactions, and in the synthesis of charge-balanced molecules. In the fractionation of muleic acid of products from substrates (i.e. provides a 100% separa ion). Through the products from substrates (i.e. provides a 100% separa ion). Through the constructed with sufficient modification due to the fact that the normally negatively charged strand is made nearly neutral It is also possible to distinguish between a enzymatically or thermally degraded DNA fragments due to the absence or presence of 3 phosphare. ABS68740-ABS68813 represent coding sequences and primers used ... the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, breast cancer, breast cancer associated protein isoform; BPI;
breast cancer associated feature; BF; diagnosis; cytostatic; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                          Composition useful for e.g. separation of nucleic acids comprises positively or neutrally charged phosphoramidite.
                                                                                                           Takova T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breast-cancer associated protein isoform BPI-46 preferred probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.0%; Score 7.8; DB 1; Lengt: 12; 81.8%; Pred. No. 1.5e+02; cive 0; Mismatches 2; Indils
                                                                                                           yamichev V, Skrzpczynski Z, Allawi HT, Wayland SR
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                                                                            INC.
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                                                                                                                                                                                                                                            Example 9; Page 71; 197pp; English
                                                                            (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2000; 2000WO-GB003143.
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30-MAR-2000; 2000GB-00007754.
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                                              06-FEB-2001; 2001US-00777430
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                                                                                                                                                          WPI; 2002-674850/72.
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hes 9; Conserv
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15-AUG-2002

The present invention describes a method for the screening, diagnosis or prognosis of breast cancer (BC), determining the stage or severity of BC, and monitoring the effect of therapy administered to a subject having BC, comprising analysing a sample of body fluid by two dimensional comprising analysing a sample of body fluid by two dimensional comprising a chosen feature whose abundance correlates with BC or predicts the onset or course of BC. The method (I) involves: (a) analysing a sample of body fluid from the subject by two-dimensional comprising a chosen feature whose relative abundance correlates with BC or predicts the onset of BC, and (b) comparing the abundance of each corporate in the sample with the abundance of that chosen feature in the sample with the abundance of that chosen feature in the sample with the abundance of that chosen feature in the sample with the abundance of that chosen feature in the sample with the abundance of that chosen feature in the sample of the stage or severity of BC, or with the abundance of an expression reference feature (BRF) in the cest sample. The method is useful for screening, diagnosis or prognosis of breast cancer, determining the stage or severity of BC, monitoring the effect of therapy administered to a subject having BC, and corporate and particular isoform (BPI) peptide ceptures of the present invention isoform (BPI) peptide cepture or exemplification of the present invention Screening, diagnosis or prognosis of breast cancer, by analyzing a sample of serum or plasma by two dimensional electrophoresis to detect the presence or level of a breast cancer-associated feature. Claim 132; Page 41; 146pp; English.

37.0%; Score 7.4; DB 1; Length 9; 88.9%; Pred. No. 16+03; cive 0; Mismatches 1; Indels Sequence 9 BP; 2 A; 2 C; 4 G; 1 T; 0 U; 0 Other; Query Match
Best Local Similarity 88.5Best Local Similarity 88.5Conservative

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ABQ71989 standard; DNA; 9 BP. ABQ71989; RESULT 276

28-AUG-2002 (first entry)

Zinc finger protein related oligonucleotide target SEQ ID NO:2287.

Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

WO200242459-A2. Homo sapiens. Synthetic. Homo

30-MAY-2002

20-NOV-2000; 2000US-00716637. 20-NOV-2001; 2001WO-US043438

(SANG-) SANGAMO BIOSCIENCES INC.

in O;

WPI; 2002-500284/53.

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.

Example 1; Page 59; 81pp; English.

the present invention centrices a zinc finger procesh. 1) that binds to a target site, comprising a first (81), a second (72), end a third (73) comprising a first (81), a second (72), and a third (73) comprises, in 3'-5' direction, a first (81), a second (82), and a third (83) target subsite. Also described are: (1) a polypeptide (11) comprising (1); (2) a polymucleotide (111) encoding (1) or (11); and (2) indescribed are: (1) a polypeptide (2) designing (M) (1) involves selecting the PI zinc finger such that it binds to the SI target subsite, and selecting the PI zinc finger such that it binds to the SI target subsite, and selecting the PI zinc finger such that it binds to the SI target subsite, thus designing (1) that binds to a target site (1) is useful for recognition of the subsite. (1) is useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in considering the expression of a target region within a subject, in the sample, and in assays to determined the phenotype and function of gene expression. (1) has improved affinity and specificity for their target sequences as well as enhanced biological activity. ABO71213 to ABO71214 and ABP48191 to ABP51230 represent DNA target sequences and zinc invention The present invention describes a zinc finger

Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Gaps .. 37.0%; Score 7.4; DB 1; Length 9; 88.9%; Pred. No. 1e+03; 1; Inde.s 0; Mismatches Query Match
Best Local Similarity 88.9
Matches 8; Conservative

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Gaps

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ABQ71918 standard; DNA; 9 BP.

(first entry) 28-AUG-2002 ABQ71918;

Zinc finger protein related oligonucleotide target SEQ ID NO:2216.

Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

Homo sapiens. Synthetic WO200242459-A2.

20-NOV-2001; 2001WO-US043438. 30-MAY-2002.

(SANG-) SANGAMO BIOSCIENCES INC. 20-NOV-2000; 2000US-00716637

Liu O;

WPI; 2002-500284/53.

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant eng.neering, comprises first, second and third zinc fingers, ordered from N- .o C-terminus.

Example 1; Page 58; 81pp; English

present invention describes a zinc finger protein (I) that binds to

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target site, comprising a first (F1), a second (F2), and a third (F3) and finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3-5 direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypebtide (II) comprising (I); (2) a polymucleotide (III) encoding (I) or (II); and (I) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, thus designing (I) that binds to that it binds to the S3 target subsite, thus designing (I) that binds to that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the mucleotide G in the 5-most position of the subsites of useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc invention
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Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

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Gaps
                                    6
37.0%; Score 7.4; DB 1; Length 9; 88.9%; Pred. No. 1e+03; cive 0; Mismatches 1; Indels
                   Local Similarity 88.5
1es 8; Conservative
       Query Match
                        Best Loc
Matches
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თ 1 ATGGACTIG 9 1 ATGGACTCG

à g RESULT 278 ABQ71988

ABQ71988 standard; DNA; 9 BP.

ABQ71988;

(first entry) 28-AUG-2002 Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

Zinc finger protein related oligonucleotide target SEQ ID NO:2286.

sapiens. Ношо

Synthetic

WO200242459-A2.

30-MAY-2002

20-NOV-2001; 2001WO-US043438

20-NOV-2000; 2000US-00716637

(SANG-) SANGAMO BIOSCIENCES INC.

Liu Q;

WPI; 2002-500284/53

useful in studying engineering, comprises N- to C-terminus. New zinc finger protein that binds to target site, gene function and for human therapeutics and plant first, second and third zinc fingers, ordered from

Designing zinc finger protein that has three zinc fingers from N-terminus and C-terminus that bind to subsites in 3' to 5' direction, in a target site, by selecting zinc fingers that bind their respective subsites.

The invention relates to a method of designing a zinc finger protein. The method is useful for designing a zinc finger protein. The method provides multi-finger zinc finger proteins with improved affinity and specificity

Disclosure, Page 24; 34pp; English

Example 1; Page 59; 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide

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(II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and binds to the S1 target subsite, selecting the F1 zinc finger such that it binds to the S2 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, may designing (I) that binds to the S3 target subsite, thus designing (I) that binds to that the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for "most position of the subsites having the nucleotide G in the 5' most position of the subsites and plant useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological actifity. ABO71213 to ABO71214 and ABP48191 to ABP51230 represent DNA target: sequences and tinc finger peptides which are given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; target sequence; zinc finger protein; multi-finger zinc finger protein; improved affinity; improved specificity; enhanced biological activity.
                                                                                                                                                                                                                                                                                Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc finger target sequence DNA #773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0126238P.
99US-0126239P.
99US-014659SP.
99US-0146615P.
2000US-00535008.
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es 8; Conservative
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                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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ADA64245 standard; DNA; 9 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Designing zinc finger protein that has three zinc fingers from N-terminus and C-terminus that bind to subsites in 3' to 5' direction, in a target site, by selecting zinc fingers that bind their respective subsites.
for their target sequences, as well as enhanced biological activity. The present sequence represents a zinc finger protein DNA target sequence.
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37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                        Score 7.4; DB 1; Length 9; Pred. No. 1e+03; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                        ds; target sequence; zinc finger protein;
multi-finger zinc finger protein; improved affinity;
improved specificity; enhanced biological activity.
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                                            Sequence 9 BP; 2 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                          Zinc finger target sequence DNA #774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 25; 34pp; English
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99US-0126239P.
99US-0146595P.
99US-0146615P.
2000US-00535008.
                                                                        37.0%;
88.9%;
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                                                                        Query Match
Best Local Similarity
                                                                                                                                                                    1 ATGGACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003068675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LIUQ/) LIU Q.
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30-JUL-1999;
30-JUL-1999;
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20-NOV-2000;
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                                                                                                                                                                                                                                                                                                             20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                               ADA64316;
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                                                                                                                                                                                                                 RESULT 280
                                                                                                           Matches
                                                                                                                                                                                                                                   ADA64316
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Designing zinc finger protein that has three zinc fingers from N-terminus and C-terminus that bind to subsites in 3' to 5' direction, in a target site, by selecting zinc fingers that bind their respective subsites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                          ds, target sequence, zinc finger protein,
multi-finger zinc finger protein, improved affinity,
improved specificity, enhanced biological activity.
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                                                                                                                                                                                                                    Zinc finger target sequence DNA #703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 24; 34pp; English.
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24-MAR-1999; 99US-0126239P.
30-ULL-1999; 99US-0146595P.
23-WAR-2000; 2000US-00535008.
20-NOV-2000; 2000US-00535008.
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Best Local Similarity
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27-MAR-1996
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ADA64245
ADA64245
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RESULT 281

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Deacon NJ,

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Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanucleotides (AAQ96406-Q97018) from the nef g ne and/or 1 or more decanucleotides (AAQ97019-Q97166) from the LTR region. The sequence of AAQ95406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The response in humans, and enable the generation of therapeutic, and immune and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                        Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanuclectides (AAQ96406-097018) from the nef gune and/or 1 or more decanuclectides (AAQ96109-097166) from the LTR region. The sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gune (AAQ96141). The response in humans, and enable the generation of their peutic, diagnostic and targeting agents against HIV-1 infection. (Update: peutic, diagnostic standardise OS field)
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            New non-pathogenic HIV-1 strain carrying a deletion is its LTR region - can be used in a vaccine to inhibit/reduse proinfection in an individual by a pathogenic strain.
                                                                                                                                                                                                                                                                                                                                    37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.68+02; ative 0; Mismatches 1; Indele
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(AURE-) AUSTRALIAN RED CROSS SOC.
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                                                                                           Claim 14; Page 197; 301pp; English
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AAQ97137 standard; DNA; 10 BP.
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94AU-00000284
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(first entry)
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Best Local Similarity
Matches 8; Conserv
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21-FEB-1994;
23-DEC-1994;
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LTR region - can be used in a vaccine to inhibit/reduce productive
infection in an individual by a pathogenic strain.
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(AURE-) AUSTRALIAN RED CROSS SOC.
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94AU-00000284.
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(first entry)
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21-FEB-1994;
23-DEC-1994;
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23-DEC-1994;
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Query Match

16-OCT-2003 27-MAR-1996

AAQ97136;

RESULT 283

Deacon NJ,

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Systemic evolution of ligands by exponential enrichmens; SELEX; therapy; random pool sequence; prophylactic; cosmetic; agricultural composition; parallel SELEX; ss.

05-NOV-1996 (first entry)

AAT28375;

DNA-PEG-malemide

Synthetic

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LTR region - can be used in a vaccine to inhibit/reduce productive
infection in an individual by a pathogenic strain.
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                                          Length 10;
                                      Score 7.4; DB 1; Length 10 Pred. No. 1.6e+02; 0; Mismatches 1; Indels
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            Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
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AURE-) AUSTRALIAN RED CROSS SOC.
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94AU-00000284.
                                       Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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23-DEC-1994;
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27-MAR-1996
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Matches
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ВЪ.

AAT28375 standard; DNA; 10

RESULT 286 AAT28375 ID AAT283

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AAT28375-T28379 represent oligomuclectides used in the method of the invention. This sequence represents a DAR-PEG-malemide sequence, which was ligated to a random pool sequence (see AAT28376) using a DNA bridge oligomuclectide (see AAT28377) to obtain a nucleic acil-reactant test mixture. The conjugate is then reacted with a second reactant test biotinylated diene prepared from NHS-blotin and 2,4-he cadien-1-ol). The products were loaded on an immobilised strength olim and the bound RNA was released by treatment with proteinase K. The fluted RNA was then reverse transcribed as in typical systemic evolution of ligands by exponential enrichment (SELEX) reactions. This process is repeated to obtain the desired product. This method can be used to identify products that bind to, or perform a preselected function on, a target sequence. The products and the methods can be used to produce therapeutic, diagnostic, prophylactic, commetic or agricultural compositions. This parallel SELEX reaction comprises forming a product library by contacting two or more reactants. The method does not require kee:ing track of a matrix of products, and does not require highly efficient or rapid matrix of products formation is directed by nucleic ac ds which when reactions. Product can be easily amplified and the product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stallel SELEX method - uses nucleic acid-reactant mixture e.g. therapeutic, diagnostic and agricultural compsns.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be reliably reproduced in subsequent rounds of projuction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Score 7.4; DB 1; Length 10; Similarity 88.9%; Pred. No. 1.6e+02; 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                            /*tag= a
/note= "FMOC-PEG-malemide labelled"
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                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 51; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV20692 standard; RNA, 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00309245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel parallel SELEX method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NEXS-) NEXSTAR PHARM INC
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gold L;
                                                                                                                                                                                                                                      Key
modified_base
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                                                                                                                                                                                                                                                                                                                                                                    28-MAR-1996.
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Matches
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ID AAV
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TAR mimetic oligonucleotide SEQ ID NO:4.

Unidentified

US5736294-A.

07-APR-1998

(first entry)

24-JUN-1998

AAV20692;

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Ecker

Vickers TA,

Bruice TW,

WPI; 1998-239195/21

(ISIS-) ISIS PHARM INC

19-MAR-1991;

91US-00724500. 90US-00497090.

27-JUN-1991;

Disclosure; Col 10; 27pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is an oligonuclectide used in a method .or coevolving products from two or more reactants, along with the nucleic acid that can facilitate the reaction for making the products. The product can have the ability to perform a preselected function on a target. The process can be used to produce having various therapeutic, prophylactic, used to produce such as pyridines. The process produces along such as pyridines. The process produces a large, structurally diverse library of products
                                                                                                                                                                                                                                                                                                       Production of a product having the ability to perform a preselected function on a target - comprises preparing a nucleic .cid test mixture, coupling with a first reactant, forming a product lib:ary, contacting with target, and partitioning the product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus; HIV; trans-acting responsive element; gene expression; viral; retroviral; infection; AIDS; mimetic; TAR; acquired immunodeficiency syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotides for modulating gene expression b_{\mathcal{Y}} RNA mimicry useful for treating viral and retroviral diseases such as AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 1.6e+02;
0; Mismatches 1; Ind.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV-1 TAR mimetic oligonucleotide loopless delTAR #2246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Col 48; 51pp; English.
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91WO-US001822.
92US-00927505.
                        96US-00618700.
                                                                               94US-00309245
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Best Local Similarity 88.9%;
Matches 8; Conservative
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                                                                                                                                    (NEXS-) NEXSTAR PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
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                                                                            20-SEP-1994;
                        20-MAR-1996;
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16-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX05660;
                                                                                                                                                                                           Gold L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is shown in the disclosure of the present invention. The present invention describes methods for interfering with HIV replication in vitro comprising: (1) contacting the vitus with an objgonucleotide (0N) or its analogue comprising the sequence (1); (2) and (3) contacting the virus with ON or its analogue comprising the sequence and a sequence selected from the group consisting of [III), [IV) and (V): 5'-CUGGGA-3' (I) 5'-CUGGGA-3' (I) 5'-NNUCNN-3' (III) 5'-NNUCNN-3' (IV) 5'-NNUCNN-3' (III) 5'-NNUCNN-3' (IV) 5'-NNUCNN-3' (IV) 8'-NNUCNN-3' (IV) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibition of HIV replication in vitro – comprises contacting virus with RNA oligo:nucleotide or its analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function; target; therapy; prophylactic; diagnosis;
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                                                                                                                                                                                           Human, placental alkaline phosphatase, PAP, gene expression, RNA, human immunodeficiency virus, HIV, TAR, mimetic, ss.
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37.0%; Score 7.4; DB 1; Length 10; 66.7%; Pred. No. 1.6e+02; Live 2; Mismatches 1; Indels

Conservative

Local Similarity Les 6; Conserv

Best Loc Matches

Query Match

14

CTCGCTGGC

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cosmetic; library; primer; ss.

US5858660-A. 12-JAN-1999

Synthetic

Product coevolution;

10mer oligonucleotide DNA

09-APR-1999

AAX01788

AAX01788 standard; DNA; 10

RESULT 288

Sequence 10 BP; 0 A; 4 C; 3 G; 0 T; 3 U; 0 Other;

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                                                                   The invention relates to defined oligonucleotides (or their analogues) that are able to mimic the secondary or tertiary structure of RNA molecules, especially mRNA. It provides specific oligonucleotides (AAXOS657-661) which mimic the human immunodeficiency virus (HIV) transacting responsive element (TAR). The RNA mimicry oligonucleotides mimic particular strands of RNA, especially mRNA, containing secondary structures important for RNA, protein interactions. The interaction of structures important for RNA, protein interactions of proteins with mimic molecules minimises the interactions of proteins with adjouncleotides are useful for regulating/ modifying gene expression and can be used in therapeutics for the treatment of viral and retroviral infections such as acquired immunodeficiency viral and research reagents, and kits. The present sequence represents a specifically claimed TAR mimetic oligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; cTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.0%; Score 7.4; DB 1; Length 10; 66.7%; Pred. No. 1.6e+02; ative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10 BP; 0 A; 4 C; 3 G; 0 T; 3 U; 0 Other;
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    Claim 14; Col 26; 22pp; English
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98US - 00898449
98US - 00899919
98US - 00899919
98US - 00899919
98US - 00899997
98US - 00900369
98US - 00900369
98US - 00900419
98US - 00900418
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Guery Match
Best Local Similarity 66.70,
Best Local Similarity 66.70,
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AAZ78047/c
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expression) tags used to identify many transcripts encoding immunostimulatory cofactor proteins which are preferentially or immunostimulatory cofactor proteins which are preferentially or immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes, particularly against tumour antigen presentation by T-cell receptors is alone activation of cytotoxic immune response that can lyse insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGI tags have several potential uses.

They may be used in vaccines to induce an immune response that can lyse consequences identified using the SAGI tags have several potential used in vaccines to induce an immune response of an APC; and as hybridisation probes/amplification privars for the capression of these genes. Detection of diseases relate to abnormal expression of these genes. Detection of the enduritic cell differentially expressed genes, or of thair encoded proteins, can be used in active immunotherapy (or to stimulate production of an end in active immunotherapy (or to stimulate production of an end in active immunotherapy (or to stimulate production of the enduringent and presentation of endogenous APCs and upregulates the AFCs for the presentation of cellinguals, migration to for estimulatory factors ensures adequate antigens and presentation of cellinguals, migrat
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98US-0090072P.
98US-0090076P.
98US-0090073P.
98US-0090080P.
98US-0111715P.
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Best Local Similarity 86.5.
Best Conservative
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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                                     19-JUN-1998;
19-JUN-1998;
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08-DEC-1998;
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ID AAZ7
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AC AAZ7
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DT 10-A
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dendritic cell SAGE tag, SEQ ID NO:546.
                         Homo sapiens.
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19-JUN-1998;
19-JUN-1998;
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19-JUN-1998;
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SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytocoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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98US-0089853P
98US-0089992P
98US-0089993P
98US-0089993P
98US-0089993P
98US-0089993P
98US-0089999P
98US-0090035P
98US-0090041P
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Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mENA transcripts encoding immunostimulatory ordactor profesins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells while preferentially or differentially expressed in dendritic cells while other transcripts correspond to novel genes. Antigen-presenting cell (APC) associated coostimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory offactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid
Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
                                                                                                                                                                                                                     Claim 1; Page 80; 130pp; English.
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98US-0090044P. 98US-0090045P. 98US-0090047P.

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They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for against a tumour antigen; to modulate the genotype of an APC; to screen for against a tumour antigen; to modulate the genotype of an APC; to screen a APC; and as hybridisation probes/amplification primers for the chapmosis, prognosis and monitoring of diseases related to abnormal chapmosis, prognosis and monitoring of diseases related to abnormal compression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins; can be used to identify calls as belonging to the monocyte lineage. Cells containing these genes can be used in active immuncherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of them antigen and presentation of co-stimulatory factors ensures adequate antigen to presentation of co-stimulatory signals, migration of chemokines for secretion of real growth factors and secretion of chemokines for recruitment of immune effector cells
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sequences identified using the SAGE tags have several potential uses
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                                                                                                                                                                                                                                                                                 Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
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9805-0089853P.
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9805-0089999P.
9805-0090035P.
9805-0090036P.
9805-0090036P.
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Best Local Similarity 88.2.
Best Local 8, Conservative
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Human dendritic cell SAGE tag, SEQ ID NO:567
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98US-0089844P.
98US-0089981P.
98US-0089991P.
98US-0089992P.
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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     Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify maNA transcripts encoding differentially expressed in monocyte-derived dendritic cells compared affectentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell other transcripts presentation by T-cell receptors is alone activation of the cytotoxic immune response, particularly against tumour cells. Immunostimulatory cofactors also being required for insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses.

They may be used in vaccines to induce an immune response, particularly against a tumour antiged, to modulate the genotype of an APC, to screen for against that modulate expression of the Genotype of an APC, and as hybridiation probes/amplification primers for the expression of the dendritic cell affermatially expressed genes, or of their encoded proteins, calls containing these genes. Detection of the dendritic cell affermation of expressed genes, or of their encoded proteins, calls containing them are used in active immunotherapy (or to stimulate production of a population of antigen-psecific effector cells and belonging to the monocyte lineage. Cells containing them are used in active immunotherapy (or to stimulate production of a population of antigen-psecific effector cells) and vectors containing them are used in active immunotherapy (or to stimulate the are used in general product factors e
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98US-0090048P.
98US-0090072P.
98US-0090077P.
98US-0090078P.
98US-0090079P.
98US-0090080P.
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Matches

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Sequences AAZ77573-Z79709 represent SAGE (serial analy is of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in moncyte-derived dendritic cells compared with moncoytes. Some of the transcripts correspond to inown genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated coetimulatory factors play an important role in the activation of the cytctoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major listocompatibility complex) and subsequent recognition by T-cell receptor listocompatibility insufficient to activate a robust cytctoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for
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SAGE tag, serial analysis of gene expression, antigen-presenting cell, APC; moncoyte-derived dendritic cell, differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte, tumour antigen; immunotherapy; anticancer; ss.
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efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the can appear, prognosis and monitoring of diseases related to abnormal expressed genes. Detection of the dendritic cell differentially cypressed genes. Detection of the dendritic cell differentially carbesed genes, or of thair encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a popularison of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of immune effector cells
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98US - 0089991P
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AAZ78796
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Sequences AAZ/15/2-2/10/10/ represent SAGE Vertical analysis of Sene Sequences AAZ/15/2-2/10/ represent SAGE Vertical analysis of Sequences AAZ/15/2-2/10/ represent SAGE Vertical SAGE 
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Pred. No. 1.6e+02;
0; Mismatches 1; Indils
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                                                                                                                                                                                                                                                                                                                                                                                                                      cells, useful in gene vaccines against cancer.
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                98US-0090048P.
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Best Local Similarity 88.9%;
Matches 8; Conservative
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                                                                                                                                                                                                                   GENZYME CORP.
ROBERTS B L.
SHANKARA S.
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              19-00N-1998;
19-00N-1998;
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19-00N-1998;
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(ROBE/)
(SHAN/)
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AAZ77705
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GENZYME CORP. ROBERTS B L.
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                                     Homo sapiens
                                            WO9965924-A2
                                                                                19 - UN 1998;
19 - UN 1998;
19 - UN 1998;
19 - UN 1998;
10 - UN 1998;
19 - UN 1998;
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19 - UN 1998;
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19-JUN-1998;
19-JUN-1998;
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                                                     23-DEC-1999
                                                                                                                                                                                                                Roberts BL,
                                                                                                                                                                                                (GENZ )
(ROBE/)
                                                                                                                                                                                                        (SHAN/)
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the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses.

They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for against a tumour antigen; to modulate the genotype of an APC; to screen can APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes in expression of their encoded proteins, can be used to identify calls as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen correspondences appeared to endogenous APCs and upregulates the APCs for the Epresentation of co-stimulatory signals, migration to T cell-rich sites, secretion of I cell growth factors and secretion of chemokines for recruitment of immune effector cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.0%; Score 7.4; DB 1; Lengtl 10; 88.9%; Pred. No. 1.6e+02; ative 0; Mismatches 1; Indels
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98US-0089997P.
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Best Local Similarity
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(ROBE/) F
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                                                                                            SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                                                                                          cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss
                                                 Human dendritic cell SAGE tag, SEQ ID NO:133.
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98US-0089813P.
98US-0089812P.
98US-0089991P.
98US-0089991P.
98US-0089993P.
98US-0089993P.
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98US-0089993P.
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98US-0090041P.
    10-APR-2000 (first entry)
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Gaps

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Claim 1; Page 71; 219pp; English.

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ct hat are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ8677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcribts can be used for disquosis, prognosis, monitoring and transcripts can be used for disquosis, prognosis, monitoring and transcripts can be used to nybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for disquosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic against Host cells that produce the polypeptides or as therapeutic and isolate populations of educated, and these used for adoptive cells, e.g. cybotoxic T lymphocytes, and these used for adoptive
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                                37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                  Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Gaps

BP. AAZ81248 standard; DNA; 10 (first entry) 07-APR-2000 AAZ81248;

Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss. Metastatic breast tumour cell upregulated transcript tag #482.

99WO-US013647 WO9965928-A2. 18-JUN-1999; 23-DEC-1999

Homo sapiens

98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 98US-0090041P 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; .9-JUN-1998; 19-JUN-1998

GENZYME CORP. ROBERTS B L. SHANKARA S. (GENZ) ((ROBE/) ! Shankara S; WPI; 2000-106079/09. Roberts BL,

Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

Isolated polynucleotides differentially expressed betgeen metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and

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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These crissue (i.e. are downergulated in metastatic breast timour cells). These transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression / amplification reactions.

Compounds that modulate expression of the transcribts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of c.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raishin specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-epecific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
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98US-0089997P.
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Best Local Similarity
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19-JUN-1998;
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ8677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cities that are downregulated in metastatic breast tumour cells). These transcripts can be used for disquosis, prognosis, monitoring and transcripts can be used for disquosis, prognosis, monitoring and by standard immunoassays or hybridisation/amplification reactions. Or preferent of breast cancer, particularly where metastatic biagnosis is by standard immunoassays or hybridisation/amplification reactions. Or preferent of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression of the transcripts are potentially useful for treatment of conferences or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based conficiens. Polypeptides encoded by the transcripts are also useful in vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host produce the polypeptides or as therapeutic and isolate populations of educated, and isolate populations of educated, and these used for adoptive
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                                  Claim 1; Page 93; 219pp; English.
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 treatment of cancer
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(ROBE/) F
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Roberts BL, Shankara S;

WPI; 2000-106079/09

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Gaps

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that are preferentially transcribed in the metastatic oreast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ89342 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for hybridisation/amplification reactions. Or standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of [metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense selected cell types, of particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells, munch because of the readoutive used for adoptive cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                       Claim 1; Page 59; 219pp; English.
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98US-0080997P.
98US-0090039P.
98US-0090040P.
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nes 8; Conservative
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ROBERTS B L.
SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 GGCACGCAC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunotherapy
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(ROBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 300
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Isolated polynucleotides differentially expressed bet sen metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and

Roberts BL, Shankara S;

WPI; 2000-106079/09.

WPI; 2000-106079/09 23-DEC-1999 ò g

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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour cells. AAZ83942 to AAZ86677 represent tags corresponding to distinct transcribts that are to AAZ86677 represent tags corresponding to distinct transcribts that are corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These care downedguated in metastatic breast tumour cells). These transcribts can be used for disgnosis, prognosis, monitoring and transcribts can be used for disgnosis, prognosis, monitoring and creatment of breast cancer, particularly where metastatic. Disgnosis is by standard immunoassans or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of ceg. therapeutic genes (also riboxymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic adents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter immunched the polypeptides used for adoptive immune the second calls that produce the polypeptides can be used to expand immune them.
Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                       Claim 1; Page 140; 219pp; English.
                                                                                                                                                  treatment of cancer.
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ö Gaps ó, Score 7.4; DB 1; Length 10; Pred. No. 1.6e+02; 0; Mismatches 1; Indels Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other; 37.0%; 88.9%; CGCTGGCAC 16

CACTGGCAC 10

AAZ84731 standard; DNA; 10 BP. 07-APR-2000 (first entry) AAZ84731;

Metastatic breast tumour cell downregulated transcript tag #3965

Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Homo sapiens

WO9965928-A2

99WO-US013647 18-JUN-1999; 98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998;

GENZYME CORP. ROBERTS B L. SHANKARA S. (GENZ) ((ROBE/) !

that are preferentially transcribed in the metastatic breast tumour cells.

that are preferentially transcribed in the metastatic breast tumour cells. Adz83942

tissue (i.e. are upregulated in metastatic breast tumour cells). Adz83942

to AAZ86677 represent tags corresponding to distinct transcripts that are

to preferentially transcribed in the primary or non-metastatic breast tumour

tissue (i.e. are downregulated in metastatic breast tumour cells). These

transcripts can be used for diagnosis, prognosis, monitoring and

transcripts can be used for diagnosis, prognosis, monitoring and

transcripts can be used for diagnosis, prognosis, monitoring and

creatment of breast cancer, particularly where metastatic. Diagnosis is

transcripts and used for diagnosis, monitoring and

compounds that modulate expression of the transcripts are potentially

compounds that modulate expression of the transcripts are potentially

consciulatly an antigen-encoding sequence for use in gene or cell-based

contines. Polypeptides encoded by the transcripts are also useful in

contines, for diagnosing breast cancer and for rasing specific

antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

agants. Host cells that produce the polypeptides can be used to expand

and isolate populations of educated, antigen-specific immune effecter

colls, e.g. oytotoxic T lymphocytes, and these used for adoptive .; 0 Gaps ; 0 Score 7.4; DB 1; Length 10; Pred. No..1.6e+02; 0; Mismatches 1; Indels Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other; Claim 1; Page 164; 219pp; English. Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative treatment of cancer

2 CTTGCTGGC 10 6 CTCGCTGGC 14 g à

AAZ84972 standard; DNA; 10 BP. 07-APR-2000 (first entry) AAZ84972; RESULT 302

Human, metastatic breast tumour tissue; breast cancer, tag; primer; non-metastatic breast tumour tissue; gene therapy; an icancer; antimetastatic; vaccine; diagnosis; ss. Metastatic breast tumour cell downregulated transcrips tag #4206.

98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 99WO-US013647 WO9965928-A2 .8-JUN-1999; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; Homo sapiens 23-DEC-1999

CORP. GENZYME ((GENZ) (ROBE/)

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Claim 1; Page 175; 219pp; English.
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98US-0089997P.
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Best Local Similarity 86.3"
Loc 8; Conservative
                                                                     Roberts BL, Shankara
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GENZYME CORP. ROBERTS B L.
                                                                                                          WPI; 2000-106079/09
                                                                                                                                                                               treatment of cancer
                                    (SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy
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19-JUN-1998;
19-JUN-1998;
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(GENZ ) (ROBE/) F
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                                                                                                      Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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hes 8; Conservative
                                    Shankara S;
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                                                                                                                                             treatment of cancer
                                                                   4PI; 2000-106079/09
(SHAN/) SHANKARA S.
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19-JUN-1998;
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RESULT 303

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that are preferentially transcribed in the metastatic oreast tumour that are preferentially transcribed in the metastatic oreast tumour (1.8. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These or issue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosic, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also riboxymes or antisense sequences), particularly an antigen-encoding sequence for use in gine or cell-based contines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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Tue Jun

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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour (i.e. are upregulated in metastatic breast tumour cells). AA286577 represent tags corresponding to distinct transcribts that are to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metasitatic breast tumour cells). These crissue (i.e. are downregulated in metastatic breast tumour cells). These transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcribts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences).

Compounds that an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raishing specific antibodies (b). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells that produce the polypeptides can a used to expand and isolate populations of educated, antigen-specific immune effecter.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 166; 219pp; English.
98US-0090039P.
98US-0090040P.
98US-0090041P.
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                                                                                                          GENZYME CORP.
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SHANKARA S.
     19-JUN-1998;
19-JUN-1998;
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(ROBE/) ]
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that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
transcripts can be used for diagnosis, prognosis, monitoring and
transcripts can be used for diagnosis, prognosis, while promoters from
transcripts are modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
the transcripts are used to direct expression, in selected cell types, of
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines, Polypeptides encoded by the transcripts are also useful in
vaccines, for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides or as therapeutic
cand isolate populations of educated, antigen-specific immune effecter
calls, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy
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                                                                                                                                                                                                                                                            Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 204; 219pp; English.
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        98US-0090041P
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                            BL, Shankara
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                                                      (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                                                                                                                                                                                                                                   treatment of cancer.
                                                                                                                                                                                                             WPI; 2000-106079/09.
                                                                                                        (SHAN/) SHANKARA S.
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        19-1000-61
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AAZ84821;

Вb

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Gaps

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98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P.

19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998;

99WO-US013647

18-JUN-1999;

19-41-NDD-6

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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used to hybridisation/amplification reactions. Owngounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for use in gene or cell-based antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-epecific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
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                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 170; 219pp; English.
98US-0089853P.
98US-0089997P.
98US-0090039P.
98US-0090040P.
                                                                                                                                                                                                              Roberts BL, Shankara S;
                                                                                                                          GENZYME CORP. ROBERTS B L.
                                                                                                                                                                                                                                                    WPI; 2000-106079/09
                                                                                                                                                                                                                                                                                                                                        treatment of cancer
                                                                                                                                                                      SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunotherapy
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                                                                                                                          (GENZ )
                                                                                                                                                                      (SHAN/)
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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and

Shankara S;

BL,

Roberts

WPI; 2000-106079/09.

(GENZ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.

Claim 1; Page 183; 219pp; English.

treatment of cancer.

37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; rative 0; Mismatches 1; Indels Query Match
Best Local Similarity 88.9
Matches 8; Conservative

AAZ85384 standard; DNA; 10 BP

AAZ85384;

07-APR-2000 (first entry)

Metastatic breast tumour cell downregulated transcript tag #4618.

Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Homo sapiens

WO9965928-A2

Homo sapiens W09965928-A2

23-DEC-1999

that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour (i.e. are upregulated in metastatic breast tumour cells). AA28697 to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These crissue (i.e. are downregulated in metastatic breast timour cells). These transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and communosasys or hybridisation/amplificatic reactions.

Compounds that modulate expression of the transcripts are potentially considered to the transcripts are gotentially where metastatic of the transcripts are gotentially considered to the transcripts are gotentially considered to the transcripts are gotentially of articularly an artigen-encoding sequence for use in gene or cell-based consocines; for diagnosing breast cancer and for raising specific articularly an artigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific articularly has are used to detect the polypeptides or as therapeutic adents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-epecific immune effecter immune hereaus. ö Gaps Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss. Metastatic breast tumour cell downregulated transcript tag #5519. ö 37.0%; Score 7.4; DB 1; Lengti 10; 88.9%; Pred. No. 1.6e+02; ative 0; Mismatches 1; Indels Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other; AAZ86285 standard; DNA; 10 BP. 07-APR-2000 (first entry) Best Local Similarity 88.9 Matches 8; Conservative 9 GCTGGCACG 17 9 GCTGACACG 1 immunotherapy AAZ86285; Query Match RESULT 308 AAZ86285, ò 셤

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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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 WO9965928-A2
                                                                       .8-JUN-1999;
                                     23-DEC-1999,
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(ROBE/)
                                                                                                                                                                                                                                                              (SHAN/)
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AAZ84046/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 204; 219pp; English,
                                                                   98US-0089853P.
98US-0089997P.
98US-0090039P.
98US-0090040P.
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                                     99WO-US013647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 88.5
                                                                                                                                                                                                                                                              Roberts BL, Shankara S;
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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                                                                                         19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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                                   18-JUN-1999;
23-DEC-1999
                                                                         9-JUN-1998
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Homo sapiens

RESULT 309
AAZ85204
XX
AC AAZ8526
AC AAZ8526
DT 07-APRXX
XX
Human,
XM
Human,
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NOn-met
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Matches

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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour cells). AAZ88677 represent tags corresponding to distinct ranscribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These tissue (i.e. are downerspilated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used to the transcripts are potentially useful for treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are seed to direct expression, in selected cell types, of e.g. therapeutic genes (also riboxymes or antisense siquences), particularly an antigen-encoding sequence for use in gene or cell-based continues. For diagnosing breast cancer and for raisin, specific antibodies (Ab). Ab are used to detect the polypeptids or as therapeutic agents. Host cells that produce the polypeptids can be useful in and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 178; 219pp; English.
                                                         98US-0089853P.
98US-0089997P.
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98US-0090040P.
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99WO-US013647
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Best Local Similarity 88.5.
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23-DEC-1999

19-JUN-1998

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antimetastatic; vaccine; diagnosis; ss.
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98US-0089997P.
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AAZ85659 Btandard; DNA; 10 BP.
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ROBERTS B L.
SHANKARA S.
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Best Local Similarity
Matches 8; Conserv
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                                   Homo sapiens
                                                                  WO9965928-A2
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(ROBE/) I
(SHAN/) 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 146; 219pp; English.
                                                                                                                                 98US-0089853P.
98US-0089997P.
98US-0090039P.
98US-0090040P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ81436 standard; DNA; 10 BP
                                                                                                99WO-US013647
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Best Local Similarity 88.2
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                               Shankara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 CTGGCACGC 18
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                                                                                                                                                                                                                                         GENZYME CORP. ROBERTS B L.
                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancer.
                                                                                                                                                                                                                                                                          SHANKARA S.
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-106079/09
                                                                                                                                                  19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
Homo sapiens
                                 WO9965928-A2
                                                                                                  18-JUN-1999;
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Roberts BL,

(GENZ) (ROBE/) (SHAN/)

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that are preferentially transcribed in the metastatic breast tumour cells.

that are preferentially transcribed in the metastatic breast tumour cells. AAZ89342

to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts are used to direct expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell-types, of e.g. therapeutic genes (also ribozymes or antisense sequences) particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
Isolated polymucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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llarity 88.9%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
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ID AAZ8
XX
AC AAZ8
XX
DT 07-A
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Human, metastatic breast tumour tissue, breast cancer, tag, primer, non-metastatic breast tumour tissue, gene therapy, anticancer,

Metastatic breast tumour cell upregulated transcript tag #670.

AAZ81436;

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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ8657 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). Preferentially transcribed in the primary or non-metastatic breast tumour cells transcripts care downregulated in metastatic breast tumour cells). These transcripts care be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cents.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Human, metastatic breast tumour tissue; breast cancer; tag; primer;
non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 189; 219pp; English.
                                                                                                                                                                                               98US-0089853P.
98US-0089997P.
98US-0090039P.
98US-0090040P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.0%;
                                                                                                                                                                  99WO-US013647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                  (GENZ ) GENZYME CORP.
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 TGGCACACA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer
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                                                                                                                                                                                                                               19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                                                                                                  WO9965928-A2
                                                                    Homo sapiens
                                                                                                                                                                  18-JUN-1999;
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AAZ81131/C
ID AAZ811
XX
AC AAZ811
XC AAZ811
XX DT 07-APR
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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ80977 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-meta-static breast tumour cells). Preferentially transcribed in the primary or non-meta-static breast tumour cells or issue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also riboxymes or antisense siquences), particularly an antigen-encoding sequence for use in jene or cell-based contines, for diagnosing breast cancer and for raisin, specific antipodies (Ab). Ab are used to detect the polypeptids or as therapeutic agents. Host cells that produce the polypeptids can as therapeutic and isolate populations of educated, and these used for adoptive calls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                             Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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.ag #365.
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
 Metastatic breast tumour cell upregulated transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 68; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                   98US-0089853P.
98US-0089997P.
98US-0090039P.
98US-0090040P.
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88.9%;
                                                                                                                                                                                                        99WO-US013647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Roberts BL, Shankara S;
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ROBERTS B L.
SHANKARA S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-106079/09.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy
                                                                                                                                    409965928-A2
                                                                                                                                                                                                    18-JUN-1999;
                                                                                                                                                                                                                                     19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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                                                                                                                                                                       33-DEC-1999
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(SHAN/)
                                                                                                                                                                                                                                                                                                                                              (GENZ )
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Matches
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AAZB3254
ID AAZB
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AC AAZB
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Tue Jun

Human macrophage gene Tag oligonucleotide sequence SE(ID NO:458

07-SEP-2000 (first entry)

AAA56564;

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Human, metastatic breast tumour tissue; breast cancer; tag; primer;
non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
             Metastatic breast tumour cell upregulated transcript tag #2488.
                                                                                                          98US-0089997P.
98US-0090039P.
98US-0090040P.
98US-0090041P.
                                                                                                    98US-0089853P
                                                                                        99WO-US013647
(first entry)
                                                                                                                                                                   Shankara S;
                                                                                                                                         GENZYME CORP.
ROBERTS B L.
SHANKARA S.
                                                                                                                                                                                WPI; 2000-106079/09.
                                                                                                                                                                                                                                                                                                                                                                  mmunotherapy
                                                   Homo sapiens
                                                              409965928-A2
                                                                                        18-JUN-1999;
                                                                                                          19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
07-APR-2000
                                                                           23-DEC-1999,
                                                                                                     19-JUN-1998
                                                                                                                                                                   Roberts BL,
                                                                                                                                         (GENZ)
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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ8667 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). AAZ83942 transcribts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for the transcripts are potentially by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially cuseful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antisen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-encoditic immune effecter cannot be used to expand and isolate populations of educated, antigen-epocific immune effecter cannot be used for adoptive
                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
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0
                           Score 7.4; DB 1; Length 10;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
Sequence 10 BP; 2 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
                           37.0%;
                        37.0
Dest Local Similarity 88.9
Matches 8; Conservative
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12 GGCACGCAC 20 1 GGCAGGCAC 9 ठ

AAAS6S64/c ID AAAS6S XX RESULT 315

琚. AAA56564 standard; DNA; 10

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The present invention describes 100 human genes, which are expressed most frequently in human monocytes. The CDNA of each gene has a sequence fully defined in the specification, and lacking the CATG sequence foulty adjacent to polyA region. Also described are: (1) an antibody cajacent to polyA region. Also described are: (1) an antibody of specifically for the protein encoded by any of the genes; (2) oligonucleotides obtained from the cDNA sequences; (3) 380 human genes which are expressed most frequently in human macrophages, differentiated from human monocytes by granulocyte-macrophage colony-stimulating factor, the CDNA of each gene has a fully defined sequence, given in the specification, lacking the base sequence. CATG located most closely to the specification, lacking the base sequence CATG located most closely to the poly A region; (4) an antibody specifically for the protein encoded by any of the genes of (3); and (5) oligonucleotides obtained from the cDNA sequences of (3); and disease onset mechanism e.g. oncogeness, genetic genesic diseases, drug development and diagnosis. AAAS6107 to AAAS6586 represent specifically claimed oligonucleotide tag sequences for human genes conset macrophages conset macrophages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes most frequently expressed in human monocytes and GM-macrophages and M-macrophages studied and with cDDNAs characterized, for study of gene specificity, disease onset mechanism, drug development and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parallel selex; diagnosis; pharmaceutical; agricultural; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                       Human, monocyte, macrophage, GM-macrophage; M-macrophage; tag; stanulocyte-macrophage colony-stimulating factor; characterisation; GM-CSF; identification; diagnosis; gene specificity; cucogenesis; disease onset mechanism; genetic disease; drug develo; ment; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hashimoto S, Matsushima K, Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 49; Page 130; 138pp; Japanese.
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                                                                                                                                                                                                                                                                         WO200024892-A1.
                                                                                                                                                                                                                                                                                                                                                            28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1998;
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                  04-MAY-2000.
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Synthetic

Eaton B,

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The present invention describes an isolated nucleic add molecule (I) consisting of a cis-acting mRNA transport sequence (RFS) (Ia) of a myelin basic protein (MBP) cDNA or its portion that enhances transport of mRNA within the cytoplasm, or consisting of a cis-acting mRNA localisation enhancer (RLE) (Ib) of MBP cDNA or its portion which anhances localisation of mRNA within the cytoplasm. (I) placed 5' or 3' to a
                                                                                                                                                     Identifying one or more sequences of a target nucleic acid (NA), useful for parallel analyses, comprises contacting the NA wish a set of pools of probes comprising mixture of probes with different insormation regions.
                                                                                                                                                                                                                                                                                                                The present sequence is a probe used to demonstrate the method of the invention, which is concerned with the use of pools of probes to enable sequencing by hybridisation, a process known as SBH. Overlapping probes are used which allows the identification of sequences longer then the probe length, and either the target unucleic acid or the probe is labelled. The method of the invention is useful for assembling sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule having cis-acting mRNA transport sequence or localization enhancer which enhance transport or localization of mRNA within cytoplasm, respectively, is useful for enhancing gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myelin basic protein; MBP; cis-acting mRNA transport sequence; RTS; cis-acting mRNA localisation enhancer; RLE; gene therapy; localisation; transport; translation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myelin basic protein consensus RTS decanucleotide #2 SEQ ID NO:32.
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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                                                Cooke
                                                                                                                                                                                                                                                                  Disclosure; Page 54; 196pp; English
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                                                Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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Best Local Similarity 88.2
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                                                   Drmanac
                                                                                                       WPI; 2000-475839/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 TGGCACGCA
HYSE-) HYSEQ INC.
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                                                   Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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AAH21642/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method has been developed for producing a product having the ability to perform a preselected function on a target. The method can be used for identifying products capable of performing a preselected function on a target. The products identified of the product a paramaceutical compositions, diagnostic reagents, agricultural compositions or manufacturing compositions. The mucleic acid that specifically facilitates the desirable product formation can be easily amplified and the product reliability reproduced in subsequent rounds of production. This method allows a multitude of reactions to take place initially which can be sorted out later once it has been determined that products which display predetermined desirable characteristics have been formed. Using the method, products may be selected for, in the absence of detailed structural information. The present sequence represents an account of the present sequence represents an account of the present sequence represents and product and products may be ablested for, in the absence of detailed and account of the present sequence represents and product and products may be ablested for, in the absence of detailed and account of the present sequence represents and product and products may be ablested for, in the absence of detailed and product and products may be ablested for, in the absence of detailed and products may be ablested for in the absence of detailed and product and products may be ablested for in the absence of detailed and product and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New method for identifying products which act on a target, useful for identifying products for use in e.g. pharmaceutical, diagnostic, agricultural and manufacturing compositions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structural information. The present sequence represents an oligonuclectide which is used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                         Tarasow TM;
target; function; ss
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Matches 8; Conserv
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Synthetic

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Query Match

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heterologous gene that is operably linked to a 5' regulatory region and a 3' termination sequence, in an expression vector is useful for expressing a heterologous gene which involves transforming a host cell with the expression vector. (I) confers properties such as localisation, transport and increased translation efficiency of a heterologous mRNA transcript when transcribed into such mRNA. (I) present in a vector is useful for increasing translation of a heterologous gene, by which increased production of recombinantly produced proteins in vivo on either a small, research scale or on a large commercial scale is increased. The recombinantly produced proteins whose translation is enhanced by (I) may be a biologically active protein, structural or therapeutic protein. (I) is useful in gene therapy. The present sequence represents an MBP consensus RTS decanucleotide sequence which is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to haplotyping the FK506-binding protein 8 (38kD) (FKBP8) gene in an individual. The method involves determining the identity of the nucleotide pair at one or more polymorphic sites selected from P1 to P26 (described in the specification). The invention is useful to improve the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with FKBP8 activity, for example immunosuppression and cancer. Sequences PA167352-403 represent oligonocleotide primers for detecting FKBP8 gene polymorphisms by primer extension techniques
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                                                                                                                                                                                                                                                                                               Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
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Best Local Similarity
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Stephens JC;
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Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

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                              Gaps
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   Lengtl: 10;
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                              Indels
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 Score 7.4; DB 1; L. Pred. No. 1.6e+02; O; Mismatches 1;
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                                                                                                                                                         AAI67391 standard; DNA; 10 BP.
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Stephens JC;
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   37.0%;
88.9%;
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Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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AA167386/c
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The invention relates to haplotyping the FK506-binding protein 8 (38kD) (FKBP8) gene in an individual. The method involves determining the identity of the nucleotide pair at one or more polymorphic sites selected from P1 to P26 (described in the specification). The invention is useful to improve the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with FKBP8 activity, for example immunosupression and cancer. Sequences PA167352-403 represent oligonicleotide primers for detecting FKBP8 gene polymorphisms by primer extension techniques
                                                                                                                                                                                                                                                                                                                                                   New haplotypes of the FK506-binding protein 8 gene, useful for genotyping that gene in individual and to design new therapy for associated disease such as immunosuppression and cancer.
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                                                       FKS06-binding protein 8; FKBP8; haplotyping; polymorphism; cancer; immunosuppression; human; primer; 88.
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                            Human FKBP8 gene polymorphism detecting primer.
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Best Local Similarity
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cancer
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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-
AH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                                                                     New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
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n as cancer cell, comprises transcriptomes express∈d in particular
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Les 8; Conservative 0; Mismatches 1; Ind.1s
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37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; Ative 0; Mismatches 1; Indels

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Kliem SE,

Choi JY,

transcriptome, gene expression pattern, cancer, drug screening, diagnosis, cell specific gene expression, ss.

Human ubiquitously expressed transcriptome sequence SE/Q ID NO: 1227.

(first entry)

20-SEP-2001

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 cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                                 Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
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New isolated polynucleotides, useful for identifying specific cell type such as cancer cell, comprises transcriptomes expressed in particular

Claim 13; Page 67; 94pp; English.

cell types.

Kinzler KW;

Velculescu VE, Vogelstein B,

WPI; 2001-367706/38.

UNIO OUNIO JOHNS HOPKINS

24-NOV-1999;

21-NOV-2000; 2000WO-US031922.

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Homo sapiens

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diagnosis, cell specific gene expression, ss.
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37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels

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11 TGGCACGCA 19

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RESULT 325 AAH64387 ID AAH64387 standard; cDNA; 10

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expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
                                                             Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                      Claim 13; Page 70; 94pp; English.
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                            (UYJO) UNIV JOHNS HOPKINS
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AMM64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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cancer diagnosis, cell specific gene expression, ss.
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                37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 65; 94pp; English.
                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2000; 2000WO-US031922
                                                                                                                                                                                                                                                                                                               AAH64282 standard; cDNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
Query Match
Best Local Similarity 86...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                               10
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                                                                                                                                6 CICGCIGGC 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-367706/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGCAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jelculescu VE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200138577-A2
                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2001.
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Disarmed lentiviral vector such as packaging and transfer vectors that direct the synthesis of lentiviral vector transcripts and lentiviral proteins, for rapid production of recombinant lentivirus.
                                                                        Lentivirus; HIV; human immunodeficiency virus; cystic fibrosis;
Huntington's; Parkinson's; Alzheimer's disease; ss.
                                                                                                                                                                                                             Bukovsky A, Farson D,
                                                                                                                                                                                                                                                                                   Example 7; Page 42; 80pp; English.
AAC86370 standard; DNA; 10 BP.
                                                                                                                                                        26-APR-2000; 2000WO-US011097.
                                                                                                                                                                         99US-0131671P
                                     (first entry)
                                                                                                                                                                                           (CELL-) CELL GENESYS INC
                                                                                                                                                                                                            Dull T,
                                                       to make
                                                                                                                                                                                                                               WPI; 2001-007231/01
                                                                                                                    WO200066759-A1.
                                                                                                                                                                          29-APR-1999;
                                                      Linker used
                                     01-MAR-2001
                                                                                                                                      39-NOV-2000
                                                                                                                                                                                                             Naldini L,
                                                                                                  Synthetic
                   AAC86370;
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ô The present invention relates to a lentivirus transfer vector with modified 5. long terminal repeat (LTR) and 3. LTR. The vector is useful for producing a recombinant lentivirus in mammalian cells. The virus is useful for in vivo and ex vivo transfer and expression of nucleic acid sequences. The recombinant lentivirus is useful for treating HIV-infected cells, cystic fibrosis, Huntington's disease, Parkinson's disease and Alzhelmer's disease. The vector is also useful for synthesizing lentiviral vector transcripts which can be packaged and lentiviral proteins for rapid production of high titer recombinant lentivirus in mammalian cells Gaps ö Score 7.4; DB 1; Length 10; Pred. No. 1.6e+02; 0; Mismatches 1; Indels Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other; 37.0%; 88.9%; Query Match Query Match Best Local Similarity 88.33, Best Local Similarity 88.33,

AAF70422 standard; DNA; 10 BP. AAF70422;

(first entry) 20-APR-2001

Human DRD2 polymorphism detection oligonucleotide primer SEQ ID NO:165

Human; dopamine receptor D2; DRD2; polymorphism; allele specific; drug target isogene; detection; single nucleotide polymorphism; SNP; genotype, schizophrenia; Parkinson's disease; myoclonus dystonia; MD; probe; PCR primer; ss.

Homo sapiens

WO200105832-A1

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The present invention describes polymucleotides comprising single nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2). The polymucleotides may be used in assays to detect and characterise polymorphisms in DRD2 that affect its expression and activity and are involved in disorders such as schizophrenia, Parkinson's and myoclonus pystonia disorders such as schizophrenia, Parkinson's and myoclonus biological function of DRD2 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression of active and functional polypeptides. Therafore it is advantageous to detect polymorphisms in the DRD2 gene affect the expression of active and functional polypeptides. Therafore it is advantageous to detect polymorphisms in the DRD2 gene affect the polymorphisms are combined in different copies of the gene. AAF70261 to AAF70309 to AAF70304 represent human DRD2 allele specific oligonucleotide probes, and papingers which are used in the detection of DRD2 polymorphisms. AAF70405 to AAF70453 to AAF70538 represent oligonucleotide primers for the detection of human invention. AAF70453 to AAF70538 represent properties of the present invention. AAF70453 to AAF70538 represent present invention the human DRD2 gene which are used in examples from the present invention
                                                                                                                                                                                                                                                                                                         Polynucleotides comprising single nucleotide polymorphisms in the human dopamine receptor D2, useful for detecting mutations associated with, e.g. schizophrenia, Parkinson's and myoclonus dystonia.
                                                                                                                                                                                                               Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                               Nandabalan K,
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 24; 135pp; English
                                                                                                                                                                (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                 Duda A,
                                                                19-JUL-2000; 2000WO-US019644.
                                                                                                                                                                                                                 Denton RR,
                                                                                                                                                                                                                                                             WPI; 2001-091967/10.
                    25-JAN-2001
                                                                                                                                                                                                                 Chew A,
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ö 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels Local Similarity 88.9 7 TCGCTGGCA 15 9 rcccrcrcA Query Match Matches ò

Gaps

ABA83149 standard; cDNA; 10 BP. ABA83149; RESULT 331 ABA83149, X8X4X6X6X6X6X6X6X6X6X6X6X6X6X6X6X6

Ceruloplasmin (ferroxidase) ovarian tumour marker SAGE tag, #109

(first entry)

08-FEB-2002

Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; dentification; serous cystadenoma; borderline serous tumour; serous cystadenoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; undifferentiated carcinoma; olear cell adenocarcinoma; cystadenofibroma; adenofibroma; gene expression; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine; SAGE tag; ss

sapiens Homo

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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA81081-ABA81122, ABA81120, ABA81180, ABA81181 and ABA81181 The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour and being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenoma, orgenatedenocarchinoma, endifferentiated carcinoma, orgenatedenocarchinoma, endifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial naalysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are
                                                                                                                                                                                                                                                                  Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        implicated in immune response pathways, in the regulation of cell
proliferation and in protein folding, and many of these are membrane-
localised or secreted. In addition to their use as diagnostic and
                                                                                                                                                                                                                                                                                                                                                                 Claim 26; Page 41; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001 (first entry)
                                                                                                                                                                                                                               WPI; 2001-626450/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF41238;
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ö prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABA83123-ABA83169, ABA83179, ABA83181 and ABA83181 represent SAGE tags derived from the ovarian tumour marker genes of the invention Gape ö 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels Seguence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other; Query Match Best Local Similarity 88.5 Then 8; Conservative

AAF41238 standard; DNA; 10 BP.

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO: 7977.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE;

serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

40200077214-A2

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032. 16-JUN-1999;

Sherman-Baust CA, Pizer ES, Hough CD;

Morin PJ,

(USSH) US DEPT HEALTH & HUMAN SERVICES

03-APR-2001; 2001WO-US010947. 03-APR-2000; 2000US-0194336P.

WO200175177-A2 11-OCT-2001 UYJO) UNIV JOHNS HOPKINS.

Kinzler K; Welculescu V, Vogelstein B,

NPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 284; 419pp; English

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate or antifungal drugs comprising: (a) contacting a test substance which modifies the expression of antifungal drug comprising candidate antifungal drug; (3) a method (M3) for cell; and (A) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression continuous nucleotidaes of a NORF gene whose expression in a congrising contacting a phase of an open expression in a congrising contacting a yeast cell of at least 1 NORF gene whose continuous nucleotidaes of a NORF gene whose expression is affected by the class of the cell cycle of a class of drugs; the old of a least 1 NORF genes may be used to identify candidate drug as a member of expression is affected by the class of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and to identification of antifungal drugs, ARF33268 to AAF33267 represent linkers and PCR primer; used in the exemplification of the present invention.

Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Gaps ; 0 Match 37.0%; Score 7.4; DB 1; Length 10; Local Similarity 88.9%; Pred. No. 1.6e+02; es 8; Conservative 0; Mismatches 1; Indels Query Match Best Loca Matches

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AAF42074 standard; DNA; 10 BP. AAF42074; AAF42074
ID AAI
XX
AC AAI
XX
XX
XX
DT 234
XX
DE Yee

RESULT 333

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonuclectide SEQ ID NO:8813.

lhis Page Blank (uspto)

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21-DEC-2000
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Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
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Saccharomyces cerevisiae

WO200077214-A2

L4-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

SNINGO ONNO COLVO

Kinzler K; Vogelstein B, Velculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 314; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamonated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes whose expression varies by at cast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of antifungal drugs (m) send of the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a method (M3) for comprising contacting human penes which are involved in cell cycle progression of a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a cut (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell of the cell cycle. The methods may be used to identify and a markers of phases of the cell cycle. The methods may be used to identify and a markers of the semplification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention.

Seguence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Gaps o; 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; Live 0; Mismatches 1; Indels 8; Conservative Query Match Best Local Similarity Matches 8; Conserv

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4 GACTCGCTG 12

g à

RESULT 334 AAF35970

AAF35970 standard; DNA; 10 BP.

AAF35970 RXXX

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2709. (first entry) 23-MAR-2001

Yeast, Saccharomyces cerevisiae, characterisation, cell. cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag, identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Kinzler K; /elculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 96; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamontate; ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (MI) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC cantifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at lm M1; and (4) a method (M4) for identifying a candidate drug as a member of and (4) a method (M4) for identifying a candidate drug as a member of contiguous nucleotidaes of a NORF gene whose expression is affected by the class of the cell with a candidate drug and contacting expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle. The captudy, monitor and affect phases of the cell cycle, the differentially expression is affected by the class of the cell cycle. The captudy monitor and affect phases of the cell cycle. The cycle and for identification of antifungal drugs which affect the cell cycle cycle and for identification of antifungal drugs and proves the contaction of antifungal drugs a

Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Gaps . 0 Ouery Match 37.0%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 1.6e+02; Matches 8; Conservative 0; Mismatches 1; Indels

0

3 GGACTCGCT 11 σ 1 GGACTCGTT

RESULT 335 AAF37397/c ID AAF373

AAF37397 standard; DNA; 10 BP.

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AAF37397;
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23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4136.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Velculescu V, Vogelstein B, Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 147; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression nor not between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifurgal drugs, and (D) monitoring expression of a NORF gene whose expression of cell; and (D) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifurgal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a contiguous nucleotides of a nord and a probe which comprises as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a conticuing expression in the yeast cell with a method (M4) for identification of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and feet may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and feet identification of antifungal drugs; the differentially cycle cycle and feet identification of antimage and feet identification of antimage and feet phases of the cell cycle and feet identification of a the present invention. AAF33267 represent linkers and PCP Invention of the present invention.

Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Gaps . 0 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels 37.0 Best Local Similarity 88.9 Matches 8; Conservative

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5 ACTCGCTGG 13

à

RESULT 336

뗦 AAF40204 standard; DNA; 10

AAF40204;

(first entry) 23-MAR-2001

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6943.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame; nonannotated ORF; SAGE, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032 .6-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Jelculescu V, Vogelstein B, Kinzler K;

VPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 248; 419pp; English

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonanotated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate of antifungal drugs comprising; (a) contacting a test substance which a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at in M1; and (4) a method (M4) for identifying a candidate drug as a member of a contiguous nucleotides of a NORF gene whose expression in a method (M4) for identifying a yeast cell with a candidate drug and contacting expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially expression is affect by asset cell of at least 1 NORF genes may be used to identify candidate drugs which affect the cell cycle and tot identification of antifungal drugs. The NORF genes may be used as markers of phases of the cell cycle the cell cycle and tot identification of antifungal drugs. Affect the cell cycle are mathods may be used to identify candidate drugs which affect the cell cycle are method, in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and port method, in the exemplification of the present invention.

Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Gaps ; 0 Query Match

37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels

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Page 157

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1 ATGGAGTCG 9
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AAF41236 standard; DNA; 10 BP AAF41236; RESULT 337

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7975.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; Sacrial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000

14-JJN-2000; 2000WO-US016223.

99US-00335032. 16-JUN-1999;

UNJO) UNIV JOHNS HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Sxample; Page 284; 419pp; English.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 348; 419pp; English

Kinzler K;

Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned Open reading frame, or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate and integer comprising; (a) contacting a test substance with a yeast cell; and (D) monitoring expression of a NORF gene whose expression of antifungal drug (a) contacting a test substance with a yeast cell; and (D) monitoring expression of a NORF gene whose expression of antifungal drug (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contitor and candidate drug as a member of a class of drugs having contacting a yeast cell with a candidate drug and monitor and affect the class of the call cycle, the differentially expression is affected by the class of the call cycle, the differentially expression is affected by the class of drugs. The NORF gene may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs, which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of the present invention.

AAP\$3262 to AAF\$3267 represent linkers and PCR primers used in the exemplification of the present invention. AAF41236/ XXX AAC AAF4; XXX AAF3; XXX Saccl CC Components (CC Components

Seguence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 37.0%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 1.6e+02; Matches 9; Conservative 0; Mismatches 1; Indels

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Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonamnotated ORF; SAGE, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                                             Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11162.
                                         AAF43023 standard; DNA; 10 BP.
                                                                                                                                                           14-JUN-2000; 2000WO-US016223.
                                                                                                                                                                       99US-00335032
                                                                                                                                                                                   (UYJO) UNIV JOHNS HOPKINS
                                                                 (first entry)
                                                                                                                       Saccharomyces cerevisiae.
17
           9 dereceace 1
                                                                                                                                   WO200077214-A2
                                                                                                                                                                        .6-JUN-1999;
                                                                 23-MAR-2001
                                                                                                                                               21-DEC-2000.
                                                    AAF43023;
                             RESULT 338
AAF43023
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or normnotated ORF) genes comprising a shall searial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administrating a NORF gene whose expression varies by at clast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifugal drug comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human puns which a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 comprising contacting a yeast cell involved in cell cycle progression in a class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in a class of drugs having a class of drugs. The NORF gene whose expression is affected by the class of drugs The NORF gene whose expression is affected by the class of drugs which affect the cell coll cycle and for identify candidate drug and contact may be used as markers of phases of the cell cycle. The methods may be used in the examplification of the present invention.

AAF33262 to AAF33267 represent linkers and characteribuses and por primers used in the exampled and for the present invention.

Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

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Gaps

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method, in the exemplification of the present invention

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Gaps

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Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

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37.0%;

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Tue Jun

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonanotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (3) a method (M2) for screening candidate of the cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1; where a candidate drug as a member of comprising contexting human DNA with a probe which comprises at least 10 comprising contexting human DNA with a probe which comprises at least 10 comprising contexting a yeast cell with a candidate drug and contioring expression in the yeast cell with a candidate drug and contioring expression in the yeast cell with a candidate drug and contexting a yeast cell cycle progression is affected by the class of the call cycle, the differentially expression is affected by the class of the call cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. Apf33268 to AAF33267 represent linkers and post the exemplification of the present invention
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                                                 Gaps
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  Score 7.4; DB 1; Length 10;
Pred. No. 1.6e+02;
); Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6924.
                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 247; 419pp; English
                                                                                                                                                                                                                                        AAF40185 standard; DNA; 10 BP.
37.0%;
88.9%;
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                                                                                                                                                                                                                                                                                                                         (first entry)
                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae.
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    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                        6 CTCGCTGGC
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                                                                                                                                                                                             RESULT 339
AAF40185/c
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression or varies as in M1, where a test substance which modifies the expression of comprising contacting human DNA with a probe which comprises at least 10 comprising contacting a wast call cover a candidate antifungal drug; (3) a method (M4) for identifying a candidate drug as a member of contacting expression in a yeast cell of at least 1 NORF gene whose expression in a yeast cell comprising contacting a yeast cell with a candidate drug and contacting expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle. The open and be used to study, monitor and affect phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle of cycle and for identification of antifungs drugs drugs which affect the cycle of cycle cycle and for identify candidate drugs where 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotaged ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
               Score 7.4; DB 1; Length 10;
Pred. No. 1.6e+02;
0; Mismatches 1; Indols
                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11918.
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                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                AAF43779 standard; DNA; 10
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Query Match
Best Local Similarity 88...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae.
                                                                                                                     11 TGGCACGCA 19
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                                                                                                                                                                                                                                                                                                                                               AAF43779;
                                                                                                                                                                                                                                              RESULT 340
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonanoctated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drug comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a yeast cell comprising contacting a yeast cell with a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose expression in a yeast cell of a least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to strudy, monitor and affect phases of the cell cycle, the differentially
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represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                    Seguence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                       37.0%; Score 7.4; DB 1;
88.9%; Pred. No. 1.6e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinzler K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF35822 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vogelstein B,
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Best Local Similarity 88.9
Matches 8; Conservative
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamotated.ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drug comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression carries as in M1, where a test substance which modifies the expression comprising contexting human panes which a probe which comprises at least 10 comprising contexting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and
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expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame; nonannotated ORF; SAGE, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
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                                                                                                                                                                                                Length 10;
                                                                                                                                                                                              Match

Local Similarity 88.9%; Pred. No. 1.6e+02;

es 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7856.
                                                                                                                                                       Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinzler K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF41117 standard; DNA; 10 BP.
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Matches
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monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used as markers of phases of the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs. AAP33268 to AAP44064 represent SAGE tags used in the exemplification of the present invention. AAP33262 to AAP33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
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Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

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Score 7.4; DB 1; Length 10;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
 37.0%;
88.9%;
Query Match
Best Local Similarity 88.9
Matches 8, Conservative
                                                     1 ATGGACTCG 9
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Gaps

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AAF39261 standard; DNA; 10 AAF39261;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6000. (first entry) 23-MAR-2001

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS

Velculescu V, Vogelstein B,

Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 214; 419pp; English

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonanotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, 5 phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human pnA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1;

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M.) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and 62/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 113; 419pp; English.

Kinzler K;

Vogelstein B,

/elculescu V,

WPI; 2001-061874/07.

99US-00335032.

16-JUN-1999;

UYJO) UNIV JOHNS HOPKINS

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        relates of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene whose to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of attrifungal drugs. AAF13268 to AAF44064 represent inhers and PCR primers used in the SAGE method, in the exemplification of the present invention.
method (M4) for identifying a candidate drug as a member of a
                                                                                                                                                                                                                                 Gaps
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88.9%; Pred. No. 1.6e+02;
7ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3164.
                                                                                                                                                                           Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2000; 2000WO-US016223
                                                                                                                                                                                                                                                                                                                                                           AAF36425 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001 (first entry)
                                                                                                                                                                                                                      Best_Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                             3 GGACTCGCT 11
                                                                                                                                                                                                                                                                                     9 GGACTCGGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200077214-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-2000
    ๙
                                                                                                                                                                                                                                                                                                                                                                                       AAF36425;
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                  RESULT 344
                                                                                                                                                                                                                                                                                                                                               AAF36425,
                                                                                                                                                                                                                                                                                                                                                              8
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comprising human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to testudy, monitor and affect phases of the cell cycle. The methods may be used as markers of phases of the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 cepresent SAGE tags used in the exemplification of the present invention. AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

0; Gaps 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; ative 0; Mismatches 1; Indels Query Match
Best Local Similarity 88.9
Matches 8; Conservative

1 ATGGACTCG 9 ATTGACTCG 1

g

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11331.

Kinzler K;

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 354; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast RESULT 345
AAF43192 standard; DNA; 10 BP.
XX
AC AAF43192;
XX
DT 23-MAR-2001 (first entry)
XX
DT 23-MAR-2001 (first entry)
XX
Yeast NORF gene SAGE tag oligonum
XX
Yeast; Saccharomyces cerevisiae;
XX
Northandranalysis of gene expression
XX
Saccharomyces cerevisiae.
XX
XX
Saccharomyces cerevisiae.
XX
XX
XX
Y
14-JUN-2000; 2000W0-US016223.
XX
XX
Y
14-JUN-1999; 99US-00335032.
XX
Y
16-JUN-1999; 99US-00335032.
XX
Y
16-JUN-1999; 99US-00335032.
XX
Y
Yeast gene coding sequences comp
PT
Yeast gene coding sequences comp
PT
Yeast gene coding sequences comp
PT
The present invention describes
CC
Coding sequence of a yeast gene
CC
Comprising a SAGE (serial analys
CC
Comprising a SAGE (serial analys
CC
Comprising a SAGE (serial analys
CC
Comprising administering a
CC
Cleast 10% between any two phases
CC
C phase, 20 phase and G2/M; (2) a metifungal drugs comprising: (a)

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cell; and (b) monitoring expression of a NORF gene whose expression cares as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a mathod (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cyeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene whose cut of the unitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. Ash3328 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Gaps ö 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.66+02; rative 0; Mismatches 1; Indels Query Match Best Local Similarity 88.9 Matches 8; Conservative

ö

11 TGGCACGCA 19 TTGCACGCA

RESULT 346

AAF43700 standard; DNA; 10 BP.

AAF43700;

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11839.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032. 16-JUN-1999;

UYJO) UNIV JOHNS HOPKINS.

Velculescu V, Vogelstein B, WPI; 2001-061874/07.

Kinzler K;

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monicoring and affecting phases of the cell cycle.

Example; Page 372; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotates! ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (MI) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at

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chast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression to yeast gene is a candidate antifungal drug; (3) a method (M3) for cheristying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in a class of drugs and place of the class of drugs and and affect phases cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle and for identification of antifungal drugs. Aspi3268 to AAF44064 cepresent SAGE tags used in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Gaps ô 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 88.> 2 TGGACTCGC 10 8

ö

1 TTGACTCGC 9

AAF41118 standard; DNA; 10 엄

ВР.

23-MAR-2001 (first entry) AAF41118;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7857.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

SNING OUND (OLYU)

Velculescu V, Vogelstein B,

Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and gene expression (SAGE) tags, useful affecting phases of the cell cycle.

Example, Page 280; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes

comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S bhase and G2/M; (2) a method (M2) for screening candidate antifungal dargs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal darg; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a class of drugs having a characteristic effect on gene expression in a class of drugs wing contacting a yeast cell with a characteristic effect on gene expression in the yeast cell order expression of antifungal drugs. The NORF gene whose expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle are persent SAGE tags used in the exemplification of the present invention.

ARF3362 to AAF33267 represent linkers and pCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Gaps .; 0 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels Local Similarity 88.9 Query Match

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1 ATGGACTCG 9 ATGCACTCG 1

ઠ 원 RESULT

AAF43100 standard; DNA; 10 BP.

AAF43100;

(first entry) 23-MAR-2001 Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11239.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotaced ORF, SAGE; serial analysis of gene expression; antifungal, tag; identification; linker, PCR primer, ds.

Saccharomyces cerevisiae.

40200077214-A2.

1-DEC-2000

14-JUN-2000; 2000WO-US016223. 99US-00335032. 16-JUN-1999;

SNING OF THE SURE HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 351; 419pp; English

Example; Page 361; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamonated ORF) genes comprising a sasigned open reading frame, or nonamonated ORF) genes comprising a sasigned open reading frame, or nonamonated ORF) genes comprising a morphod (M1) of using NORF genes to affect the cell cycle comprising administering an NORF gene whose expression varies by at cell fundal darge comprising of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal darge comprising expression of a NORF gene whose expression of the yeast gene is a candidate antifungal darge of (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the cell; and (b) monitoring expression of a nord (comprising contacting human DNA with a probe which comprises at least 10 contacting human genes which are involved in cell cycle progression in a comprising contacting them a nord confider of the safet of the cell of a contity and comprising contacting a characteristic effect on gene expression in a contitoring expression in the yeast cell of at least 1 NORF gene may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. As and in the SAGE represent invention.

AAP33262 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention.

Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Gaps . 0 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels Best Local Similarity 88.8 Matches 8, Conservative Query Match

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4 GACTCGCTG 12

8

GACTCGTTG 10

RESULT 349

23-MAR-2001 (first entry) AAF43372;

AAF43372 standard; DNA; 10 BP

feast NORF gene SAGE tag oligonucleotide SEQ ID NO:11511.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag, identification, linker, PCR primer, ds.

Saccharomyces cerevisiae

WO200077214-A2.

14-JUN-2000; 2000WO-US016223. 21-DEC-2000.

99US-00335032 16-JUN-1999;

Kinzler K; Velculescu V, Vogelstein B, (UYJO) UNIV JOHNS HOPKINS.

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotatud ORP) genes comprising a SAGE (serial analysis of gene expression; tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate or antifungal drugs comprising: (a) contacting a test substance which expression of the yeast gene is a candidate antifungal drug; (3) a method (M2) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M2) for cell; and (b) monitoring expression of a NORF gene whose expression of comprising contacting human DNA with a probe which comprises at lm M1, contiguous nucleotidates of a NORF gene whose expression in a contiguate and a member of a class of drugs having a characteristic effect on gene expression in a contiguate and probe which affect the cell contiguous nucleotidate of a paracteristic effect on gene expression in a contracting a yeast cell with a candidate drug and contacting expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially expression in the yeast cell of at least 1 NORF genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. ARF33268 to AAF33267 represent lankers and PCR primers used in the exemplification of the present invention.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
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8 CGCTGGCAC 16 à 쉱

0

AAF40677 standard; DNA; 10 BP. RESULT 350 AAF40677

AAF40677;

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7416.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame; nonannotated ORF; SAGE, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering administering a NORF gene whose expression varies by at cate through drugs comprising a NORF gene whose expression varies by at anithurgal drugs comprising; (a) contacting a test substance with a yeast call; and (b) monitoring expression of a nithurgal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a northing a candidate anithurgal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially cortacting any be used as markers of phases of the cell cycle. The methods may be used to identify admiddate drugs which affect the cell cycle and for identification of antifungal drugs. Apr33268 to AAF33262 represent invention. AAF33262 to AAF33267 represent invention of the present invention. AAF33262 to AAF33267 represent invention of the present invention. Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Example; Page 264; 419pp; English.

Gaps . 0 Score 7.4; DB 1; Length 10; Pred. No. 1.6e+02; 0; Mismatches 1; Indels Seguence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other; 37.0%; 88.9%; 8; Conservative Query Match Best Local Similarity Matches 8; Conserv

4 GACTCGCTG 12

AAF38331 standard; DNA; 10 (first entry) 23-MAR-2001 AAF3831;

ВР.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5070.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JJN-2000; 2000WO-US016223

99US-00335032

.6-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 181; 419pp; English

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamotetria ORF) genes comprising a shall analysis of gene expression; tag. Also described are: (1) a method (M1) of using NORF gene whose expression varies by at cycle comprising administering a NORF gene whose expression varies by at clast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drug comprising expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying a candidate drug as member of a comprising contacting human DNA with a probe which comprises at least 10 comprising contacting a yeast cell inth a candidate drug and conticting expression in a class of drugs having a characteristic effect on gene expression in a characteristic effect on gene expression in a cypression is affected by the class of the cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle. The methods may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF33267 represent in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR pinners used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Gaps ·. 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; 1; Indels 0; Mismatches Local Similarity 88.9 nes 8; Conservative Matches

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11 TGGCACGCA 19

ð 셤 RESULT 352 AAS18719

AAS18719 standard; DNA; 10 BP.

AAS18719;

12-MAR-2002 (first entry)

Primer-extension oligonucleotide #7 to detect human SCYA3 polymorphisms.

Human, single nucleotide polymorphism; SNP; SCYA3; chromosome 17q11-q21; small inducible cytokine A3; haplotyping; genotyping; primer; ss; inflammatory disorder.

Homo sapiens.

40200179217-A2. 35-OCT-2001. 30-MAR-2001; 2001WO-US010595.

14-APR-2000; 2000US-0197830P.

(GENA-) GENAISSANCE PHARM INC.

A3 (SCYA3)

Stephens JC;

Choi JY, Koshy B,

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The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human small inducible cytokine A3 (SCYA3) gene located on chromosome 17g1-421, and methods for haplotyping and/or genotyping the SCYA3 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the SCYA3 gene polymorphisms. The polymucleotides and screened compounds are useful for (developing) treatment of diseases associated with SCYA3 activity, such as inflammanory disorders e.g. atopic dermatitis, rheumatoid arthritis, multiple sclerosis, pulmonary fibrosis and sarcoidosis. AASI8712-AASI8712 represent primer-extension oligonucleotides for detecting human SYCA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer-extension oligonucleotide #11 to detect human SCYA3 polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; single nucleotide polymorphism; SNP; SCYA3; chromosome 17q11-q21;
small inducible cytokine A3; haplotyping; genotyping; primer; ss;
inflammatory disorder.
                                                                            New polymorphic variants comprising small inducible cytokine A3 (SCY) isogene, useful in expressing SCYA3 protein for use in screening for candidate drugs to treat diseases related to SCYA3 activity, e.g. inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                        Claim 17; Page 15; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US010595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ACTCGCTGG 13
                                              WPI; 2002-055247/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                              gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200179217-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                Chew A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chew A,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 353
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10

Acrerered

BP.

(first entry)

New polymorphic variants comprising small inducible cytokine A3 (SCYA3) isogene, useful in expressing SCYA3 protein for use in screening for candidate drugs to treat diseases related to SCYA3 activity, e.g.

Claim 17; Page 15; 67pp; English

inflammatory disorders.

Choi JY, Koshy B, Stephens JC,

WPI; 2002-055247/07

PHARM INC

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Gaps ; 0

1, Indels

37.0%; Score 7.4; DB 1; Length 10; larity 88.9%; Pred. No. 1.6e+02; Conservative 0; Mismatches 1; Indels

.. 0 The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human small inducible cytokine A3 (SCYA3) gene located on chromosome 17q11-q21, and methods for haplotyping and/or genctyping the SCYA3 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the SCYA3 gene polymorphisms. The polymucleotides and screened compounds are useful for (developing) treatment of diseases associated with SCYA3 activity, such as multiple associated with SCYA3 activity, such as multiple sclerosis, pulmonary fibrosis and sarcoidosis. AASI8713-AASI8742 represent primer-extension oligonucleotides for detecting human SYCA3 gene polymorphisms The present invention provides the protein, gene and CDNA sequences of the human potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) isogene and polymorphisms identified within these esquences. The sequences can be used to screen drugs, which involves contacting the polypeptide with a candidate agent, and to assay for binding activity as a target for drugs to treat arrhythmia and seizures. Ine present sequence is a primer extension oligonucleotide described in the invention Isolated polymorphic variants of potassium voltage-gated channel, Shabrelated subfamily, member 1 (KCNB1) gene useful for expressing KCNB1 protein isoform to screen drugs to treat KCNB1 activity-related disease. Gaps Human, KCNB1; single nucleotide polymorphism; SNP; gene therapy;
potassium voltage-gated channel; Shab-related subfamily, member 1;
isogene; arrhythmia; seizures; allele-specific oligonucleotide; PCR; ö 17.0%; Score 7.4; DB 1; Length 10; larity 88.9%; Pred. No. 1.6e+02; Conservative 0; Mismatches 1; Indels Length 10; Human KCNB1 gene primer extension oligo SEQ ID NO: 39 Seguence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other; Seguence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other; Score 7.4; DB 1; Pred. No. 1.6e+02; primer extension oligonucleotide; ss Claim 18; Page 14; 180pp; English. ä (GENA-) GENAISSANCE PHARM INC 05-JUL-2000; 2000US-0215885P. 37.0%; 88.9%; 05-JUL-2001; 2001WO-US021307 ä AAL45325 standard; DNA; 10 (first entry) Choi JY, Koshy CTGGCACGC 18 9 WPI; 2002-188469/24. Best Local Similarity Matches 8; Conserv CTGACACGC Query Match Best Local Similarity WO200204675-A1. Homo sapiens 29-MAY-2002 17-JAN-2002. AAL45325; 10 Query Match Chew A, RESULT 354 AAL45325 8866666666666888 ઠે 셤

Tue Jun

Human, coagulation factor XII; F12; haplotyping; haplotype pair; 88; single nuclectide polymorphism; genotyping; gene therapy; drug screening; coronary artery disease; liver disease; spontaneous abortion; cardiant; Alzheimer's disease; blood coagulant; and disease; blood coagulant; neuroprotective; noctropic; coagulant; antiabortive; sequencing primer; PCR primer; probe;

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Nandabalan

Choi JY,

Chew A,

Bentivegna SC,

WPI; 2002-075061/10.

13-APR-2001; 2001WO-US012257. 14-APR-2000; 2000US-0197837P. (GENA-) GENAISSANCE PHARM INC

MO200179228-A2.

25-OCT-2001.

Ното варіеля

primer tail

Human F12 gene allele-specific oligonucleotide PCR primer #26.

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                                                                                                                                                                                                                                                   Human; single nuclectide polymorphism; SNP; IMPDH2; chromosome 3p21.2; IMP dehydrogenase 2; haplotyping; genotyping; cancer; cytostatic; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human IMP dehydrogenase 2 (IMPDH2) gene located on chromosome 3p21.2, and methods for haplotyping and/or genetypen and individual. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the IMPDH2 gene polymorphisms. The polymucleotides and screened compounds are useful for (developing) treatment of diseases associated with IMPDH2 activity, such as cancer. AASI8280-AASI830s, represent primer-extension oligonucleotides
                                                                                                                                                                                                                      Primer-extension oligonucleotide #6 to detect IMPDH2 gene polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide having polymorphic variant of IMP2 dehydrogenase gene, useful for studying expression of the gene in vivo, and for testing efficacy of therapeutic agents for cancer in biological
Gaps
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stephens JC;
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Ä
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for detecting IMPDH2 gene polymorphisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 13; 70pp; English.
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                                                                                                                                 AAS18285 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000; 2000US-0196248P.
                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2001; 2001WO-US011851
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Best Local Similarity 88.3°,
Best Local Similarity
                                                                                                                                                                                           (first entry)
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8; Conservative
                            CGCTGGCAC 16
                                                      cgcrercac 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choi JY,
                                                                                                                                                                                                                                                                                                                                            WO200177363-A2
                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                           25-FEB-2002
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                            ω
                                                                                                                                                              AAS18285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chew A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system.
Matches
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The invention relates to single nucleotide polymorphisms in the gene encoding the human coagulation factor XII (F12) polypeptide. A method for encoding the human coagulation factor XII (F12) polypeptide. A method for haplotyping the F12 gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the F12 haplotypes given to pair. This method is useful in genotyping, whereby all possible haplotype pair can be assigned to specific genotypes. An association between a pair can a haplotype or haplotype pair of the F12 gene can be identified by comparing the frequency of the haplotype or haplotype pair in of the haplotype pair in a reference population, where a higher haplotype or haplotype pair. F12 and its corresponding DNA are used for studying the expression and function of F12, for use in screening for candidate drugs to treat disorders related to F12 eacivity such as coronary artery disease, liver disease, spontaneous abortion, Alzheimer's disease and other diseases associated with defects in blood coagulation. The sequences are also useful for studying it effects in blood cagulation. The sequences are also useful for studying it effects in blood cagulation. The sequences are also useful for studying it effects in blood cagulation. The sequences are also useful for studying the effect of variation on the biological activity of F12 seeme bolymorphisms by primers and primer tails used to detect F12 gene polymorphisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated human coagulation factor XII polynucleotide, F12 useful for treatment of e.g. coronary artery disease, comprises a sequence which is a polymorphic variant of a reference sequence for F12 gene or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 14; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK93938 standard; cDNA; 10
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hes 8; Conserv
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Best Local Si
Matches 8,
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Gaps ö

AAS99299 standard; DNA; 10 BP.

GACTCGCTG 12

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GCCTCGCTG

(first entry)

12-MAR-2002

AAS99299;

RESULT 356 AAS99299/C ID AAS992: XX AC AAS992: XX DT 12-MAR.

colorectal; breast; pancreas; head and neck tumour; colid tumour; myeloproliferative disorder; leukaemia; non-Hodgkin lymphoma; shock; leukopenia; thrombocytopenia; angiogenesis disorder; kapbosi's shock; inflammatory disease; allergy; inflammatory bowel disease; sepsis; autoimmune disease; arbritis; psoriasis; asthma; thrombosis; pain; respiratory tract inflammation; organ transplantation; angina; AIDS; cardiovascular disease; hypertension; oedema; atheroscierosis; reperfusion injury; ischaemia; central nervous system disease; infection; Alzheimer; disease; diabetes mellifus; osteoporosis; gene; 521; ss; acquired immune deficiency syndrome; expressed sequence tag; BAA3445.1.

protein kinase; cell-cell adhesion; neoplasm; nelanoma; lung;

Human protein kinase BAA34445.1 expressed sequence tag (EST) #10

(first entry)

26-AUG-2002

ABK93921;

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The invention relates to a protein kinase polypeptide (I), BAA34445.1, and the encoding polynuclectide (II). (I) is useful as a protein kinase and the encoding polynuclectide (II). (I) is useful as a protein kinase are coll-cell adhesion. (II) is useful in therapy or diagnosis of disease and for treatment of neoplasm e.g. melanoma, lung, colorectal, breast, pancreas, head and neck and other solid tumours, myeloproliferative disorder, such as leukaemia, non-Hodgkin lymphoma, leukopenia, thrombocytopenia, angiogenesis disorder, Kaposi's sarcoma, inflammation, desease, such as allergy, inflammatory bowel disease, authritis, psoriasis and respiratory tract inflammation, aschma, organ transplantation, cardiovascular disease, bypertension, oedema, angina, entral nervous system disease, including Alzhainer's disease, brain injury and amyotrophic lateral sclerosis, pain, renal disease, brain injury and amyotrophic lateral sclerosis, pain, renal disease, diabetes mellitus, osteoporosis, AIDS, viral infection, bacterial infection, fungal infection and parasitic infection. ABK93911-ABK93949 represent protein kinase coding sequences and related expressed sequence tags of the invention
                                                                                                               mumani processi. Assassi cell.cell aducesson; mechanomi, mechanomi at inug; colorectal; breast; pancreas; head and neck tumour; solid tumour; myeloproliferative disorder; leukaemia; non-Hodgkin lymphoma; shock; leukopenia; thrombocytopenia; angiogenesis disorder; Kaboai's sarcoma; inflammatory disease; allergy; inflammatory bowel disease; sepsis; autoimmune disease; arthritis; psoriasis; asthma; thrombosis; pain; respiratory tract inflammation; organ transplanteation; angina; AIDS; cardiovascular disease; hypertension; oedema; atherosclerosis; reperfusion injury; ischaemia; central nervous system disease; infection; Alzheimer; disease; brain injury; amyotrophic lateral soletosis; renal disease; diabetes mellitus; osteoporosis; gene; EST; ss; acquired immune deficiency syndrome; expressed sequence tag; BAA3445.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel protein kinase polypeptide useful for treating solid tumors, inflammatory disease, autoimmune disease, arthritis, organ transplantation, cardiovascular disease, central nervous system disease,
                                                                                                    Human; protein kinase; cell-cell adhesion; neoplasm; melanoma; lung;
                                                  Human protein kinase BAA34445.1 expressed sequence tag (EST) #27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicholls RQ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-OCT-2001; 2001WO-GB004719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2000; 2000GB-00026004
26-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INPH-) INPHARMATICA LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Novel protein kinase polypeptide useful for treating solid tumors, inflammatory disease, autoimmune disease, arthritis, organ transplantation, cardiovascular disease, central nervous system disease,

Example 1; Fig 11; 94pp; English.

and infection.

Nicholls RQ;

WPI; 2002-489944/52.

(INPH-) INPHARMATICA LTD Fagan RJ, Phelps CB,

24-OCT-2001; 2001WO-GB004719. 24-OCT-2000; 2000GB-00026004.

WO200234901-A2.

32-MAY-2002

Homo sapiens.

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The invention relates to a protein kinase polypeptide (I), BAA34445.1,
and the encoding polynucleotide (II). (I) is useful as a protein kinase
and tor effecting cell-cell adhesion. (II) is useful for expressing a
protein with kinase activity. (I) and (II) are useful in therapy or
diagnosis of disease and for treatment of neoplasm e.g. melanoma, lung,
colorectal, breast, pancreas, head and neck and other solid uncours,
myeloproliferative disorder, such as leukaemia, non-Hodgkin lymphoma,
leukopenia, thrombocytopenia, angiogenesis disorder, Kaposi's Sarcoma,
inflammatory disease, such as allergy, inflammatory bowel disease,
autoimmune disease, arthitis, psoriasis and respiratory tract
inflammation, oedema, angina, atheroselerosis, thrombosis, sepsis, shock,
repertusion injury, ischaemia, central nervous system disease, including
Alzheimer's disease, brain injury and amyotrophic lateral sclerosis,
capin, renal disease, diabetes mellitus, osteoporosis, AIDS, viral
infection, bacterial infection, fungal infection and parasitic infection.
ABK93911-ABK87919 represent to the protein kinase coding sequences and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tags of the invention
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nes 8; Conserv
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0; Gaps

ABK93921/c ID ABK93921 standard; cDNA; 10

RESULT 358

TGGCACGCA 19

11

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TGGCAGGCA 2

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Pyridoxal kinase; pyridoxine; vitamin B6; PDXK autoimmune polyglandular disease type 1; transgenic animal; gene therapy; primer extension; primer; ss.

40200190125-A2. Homo sapiens.

Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) primer #29

26-MAR-2002 (first entry)

ABK17006;

ABK17006 standard; DNA; 10 BP.

RESULT 360 ABK17006

10 TGGCAGGCA 2

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Human; protein kinase; cell-cell adhesion; neoplasm; melanoma; lung; colorectal; breast; pancreas; head and neck tumour; solid tumour; melanomicaliferative disorder; letkaemia; non-Hodgkin lymphoma; shock; leukopenia; thrombocytopenia; angiogenesis disorder; Kaposi's sarcoma; inflammatory disease; allergy; inflammatory bowel disease; sapsis; autoimmune disease; arthitis; psoriasis; asthma; thrombosis; pain; respiratory tract inflammation; organ transplantation; angina; AIDS; cardiovascular disease; hypertension; oedema; atherosclerosis; pain; reperfusion injury; ischaemia; central nervous system disease; infection; Alzheimer's disease; brain injury; amyotrophic lateral acterosis; renal disease; diabetes mellitus; oetecporosis; gene; EST; ss; acquired immune deficiency syndrome; expressed sequence tag; BAA3445.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel protein kinase polypeptide useful for treating solid tumors, inflammatory disease, autoimmune disease, arthritis, organ transplantation, cardiovascular disease, central nervous system disease,
                                                                                                                                                                                                                                                         Human protein kinase BAA34445.1 expressed sequence tag (EST) #38.
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                   949/c
ABK93949 standard; cDNA; 10 BP
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                                                                                                                                                                                       26-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-489944/52.
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                                                                                                                 ABK93949;
ABK91949/C
XX ABK91
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The invention relates to a protein kinase polypeptide (I), BAA34445.1,
and the encoding polynucleotide (II). (I) is useful as a protein kinase
and the encoding polynucleotide (II). (I) is useful as a protein kinase
and for effecting cell-cell adhesion. (II) is useful in therapy or
diagnosis of disease and for treatment of neoplasm e.g. melanoma, lung,
colorectal, breast, pancreas, head and neck and other solid tumours,
myeloproliferative disorder, such as leukaemia, non-Hodgkin lymphoma,
leukopenia, thrombocytopenia, angiogenesis disorder, Kaposi's sarcoma,
inflammatory disease, such as allergy, inflammatory bowel disease,
inflammation, asthma, organ transplantation, cardiovascular disease,
inflammation, oedema, angina, atherosolerosis, thrombosis, sepsis, shock,
reperfusion injury, ischaemia, central nervous system disease, including
Alzheimer's disease, brain injury and amyotrophic lateral sclerosis,
pain, renal disease, brain injury and amyotrophic lateral sclerosis,
pain, renal disease, brain injury and amyotrophic lateral sclerosis,
infection, bacterial infection, fungal infection and parasitic infection.
ARK93911-ABK3394 represent protein kinase coding sequences and related
expressed sequence tags of the invention
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8 CGCTGGCAC 16
              CGCTGGCTC 10
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Gaps

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Query Match
37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels

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The invention describes an isolated human pyridoxal (pyridoxine, vitamin B6) Kinase, (PDXK) polynucleotide. The polynucleotide is useful in studying the expression and function of PDXK, and in expressing PDXK protein for use in screening for candidate drugs to treat PDXK related diseases and for therapeutic purposes. A transgenic animal is useful for studying expression of the PDXK isogenes in vivo, for in vivo screening and testing of drugs targeted against PDXK protein, and for testing the efficacy of therapeutic agents and compounds for autoimmune polyplandular disease type I. The polypeptide is useful for studying the effect of the variation on the biological activity of PDXK and the binding affinity of candidate drugs targeting PDXK for the treatment of autoimmune polyglandular disease type I. Genotyping and haplotyping is useful for improving the efficacy and reliability of several steps in the discovery and development of drugs for treating diseases associated with PDXK as a candidate agent for treating diseases type I, to validate PDXK as a candidate agent for treating a specific condition or disease clinical trials of candidate drugs. This sequence is one of 38 (see ABK16978-ABK17015) primers used for detecting PDXK gene polymorphisms by primer extension texminates, described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNts, useful for therapeutic purposes, for studying the expression and function of the polyNt, and for expressing pyridoxal protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Page 14; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                24-MAY-2001; 2001WO-US016909.
                                                                                                                                                                                                                                                                                                                                                        24-MAY-2000; 2000US-0206664P.
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Best Local Similarity 88.9
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Duda A, Koshy
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                                                                                                                                                                                                                                                                          29-NOV-2001.
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AAL48062/c
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11 TGGCACGCA 19

AAL48062 standard; DNA; 10 BP.

(SANG-) SANGAMO BIOSCIENCES INC 20-NOV-2000; 2000US-00716637.

WPI; 2002-500284/53.

20-NOV-2001; 2001WO-US043438

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The present invention provides the protein, gene and cDNA sequences of human colony stimulating factor 3(granulocyte) CSF3. Also described are single nucleotide polymorphisms (SNPs) identified within these sequences. The sequences can be used in the treatment of neutropenia, promyelocytic leukaemia and haematological disorders. The present sequence is an allele specific primer extension oligonucleotide used to isolate the coding
                                                                                                                      Human; colony stimulating factor 3(granulocyte); CSF3; SNP; isogene; chromosome 17q11-12; single nucleotide polymorphism; immunostimulant; neutropenia; promyelocytic leukaemia; haematological disorder; gene therapy; PCR; primer extension oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                               New variants of colony stimulating factor 3 (CSF3) isogenes, useful fimproving efficiency and reliability in the development of drugs for treating diseases associated with CSF3 activity e.g. neutropenia.
                                                                                         Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc finger protein related oligonucleotide target SEQ ID NO:567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 19; Page 13; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                       (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ71448 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                           11-JUN-2001; 2001WO-US018813.
                                                                                                                                                                                                                                                                                                                        09-JUN-2000; 2000US-0210380P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences of the invention
                                                            (first entry)
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Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Duda A, Kazemi A,
                                                                                                                                                                                                                                WO200194364-A2
                                                                                                                                                                                                   Homo sapiens
                                                            27-SEP-2002
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ABQ71448/c
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Sausker EA;

Messer C,

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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) can careful site, comprising a first (FI), a second (F2), and a third (F3) careful site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (CI) comprising (I), (2) a polymudeotide (III) encoding (I) or (III); and (CI) designing (I), involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it compared to the S2 target subsite, and selecting the F3 zinc finger such that it compared to the S3 target subsite, thus designing (I) that binds to the S2 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplic target subsites (CI) that binds to useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in clinger the expression of a target region within a subject, in clinger such and in assays to determined the phenotype and function of in a sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced biological activity. ABG71213 to ABG72214 and ABB73230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                        New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     Example 1; Page 43; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ71449 standard; DNA; 10 BP.
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Gaps

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1; Indels

37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02;

0; Mismatches

WO200242459-A2

Synthetic.

Homo

30-MAY-2002

Tue Jun

(SANG-) SANGAMO BIOSCIENCES INC

Liu Q;

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The present invention describes a zinc finger protein (1) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) and a third (F3) that chinger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (M) (1) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, thus designing (I) that binds to the S2 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and the subsite of a target function of target target target subsites that the subsite of a target function, and for human therapeutic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of a farget sequences and zinc target sequences and zinc finger peptides which are given in the exemplification of the present
                                                                                                       New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRES; internal ribosome entry site; viral protein synthesis inhibition; viral replication inhibition; viral infection; virucide; IIIc loop; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus internal ribosome entry site, IRES, IIIc loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                         Example 1; Page 43; 81pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2000; 2000FR-00013303
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Best Local Similarity 88.9
Matches 8; Conservative
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/*tag=
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                                                                         WPI; 2002-500284/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FR2815358-A1
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stem_loop
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The present invention relates to a method for screening for a recombinant polypeptide, which contains at least one mutant RNA recognition motif (mRR) for binding to an internal ribosome entry site (TRS), or one of its domains. The recombinant polypeptide inhibits viral proteins synthesis (and thus viral replication) in vivo and in viro, by binding to its in competition with cellular or viral proteins that normally bind to it. Recombinant polypeptides identified by the invention are useful for treatment or prevention of viral infection in which the replication cycle includes a CAP-independent translation of an RNA sequence, appecifically hepatitis C virus, but also bovine/calf/human diarrhoea viruses swine pest, piglet transmissible gastro-enteritis, foot-andmouth disease, hepatitis A murine hepatitis, common cold virus or avian Hepatitis. The present sequence is the IIIc loop of the IRBS from Hepatitis C virus, which was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                              Screening for polypeptide having mutant RNA recognition site, useful for controlling viral infections, especially hepatitis C, by binding to internal ribosome entry site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to SAGE (serial analysis of gene expression) tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGE tag; serial analysis of gene expression; human; Th1 cell; activated T cell; T lymphocyte; immune response; expression pattern; preferential expression; immune disorder; EST; expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human activated Th1 and Th2 cell expression gene group, diagnosis and treatment of Th1 and Th2-related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 0 A; 4 C; 5 G; 0 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 19; Page 10; 60pp; Japanese
                                                                                                                                                                                Claim 8; Page 34; 40pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV78428 standard; cDNA; 10 BP.
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Best Local Similarity 88...
Best Conservative
(PART-) PARTEUROP DEV SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 GGCACGCAC 20
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                                                                       WPI; 2002-354321/39.
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                                    Balakireva L;
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ABV78428/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CXSXLLXBXBXBXBXBXBXXBXXBXBXBXBXCBXCCX
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representing 171 genes which are more highly expressed in Th1 cells compared with Th2 cells

Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

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representing groups of genes which are expressed in activated human Thi and/or Th2 cells. The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motify lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in Th1 and/or Th2 cells, antibodies against these proteins, and inhibitors of the expression of groups of genes that are expressed in either or both the two cell types. Groups of genes that are expressed in and/or Th2 cell types may be used for the diagnosis and treatment of Th1 and Th2 cells disorders. Sequences ABV78390-ABV78560 are SACE tags compared with Th2 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human activated Th1 and Th2 cell expression gene group, useful for the diagnosis and treatment of Th1 and Th2-related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAGE tag; serial analysis of gene expression; human; Th1 cell; activated T cell; T lymphocyte; immune response; expression pattern; preferential expression; immune disorder; EST; expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:217.
                                                                                                                                                                                                                                                                               37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19; Page 12; 60pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV78506 standard; cDNA; 10 BP
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Best Local Similarity 88.5-
6. Conservative
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C-induced hepaticis C (CH) liver tissue or hepatitis C-induced hepatocellular carcinoma (HCC) compared with normal human liver tissue.

The SAGE tags of this invention consist of a sequence of 10 mucleotides consist of a sequence of 10 mucleotides consist of a sequence of 10 mucleotides consist of the SAGE tags of this invention consist of a sequence of 10 mucleotides consist of the SAGE tags of this invention consist of genes. These tags serve polya region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the construction of consist of the expression in particular cell types. The invention also crelates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the chronic hepatitis C tissue or HCC may be used for the diagnosis and crivity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV94691ABV84700 are SAGE tags representing the 100 least highly expressed genes which are underexpressed in hepatocellular carcinoma compared with chronic hepatitis C liver tissue hepatocellular carcinoma compared with chronic hepatitis C liver tissue
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llarity 88.9%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 1; Indels
  Score 7.4; DB 1; Length 10;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 46; Page 27; 139pp; Japanese.
                                                                                                                                                                                                                                     ABV84790 standard; cDNA; 10 BP.
    37.0%;
88.9%;
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Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                      3 GGACTCGCT 11
                                                                                                                   1 GGAATCGCT 9
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Best Local Similarity
Matches 8; Conserv
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ABV84790
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are expressed in activated human Thi and/or Tha cells. The SAGE tags of this invention consist of a sequence of IO nucleotides located downstream of the 3-CATG-3' sequence motiflying nearest to the polya region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in Thi and/or Th2 cells, antibodies against these proteins, and inhibitors of the expression of groups of genes that are expressed in either or both the two cell types. Groups of genes expressed in Thi and/or Th2 cell types may be used for the diagnosis and treatment of Thi and /12-related disorders. Sequences ABV78390-ABV78560 are SAGE tags

(first entry)

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Human multiple chronic hepatitis C underexpressed genes SAGE tag #106.
ABV84296 standard; cDNA; 10 BP.
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  The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C induced human liver tissue.

The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the S'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the polyA region of cDNAs derived from a variety of genes. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis of liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of genes that are overexpressed in chronic hepatitis C liver tissue or HCC may be used for the diagnosis and in chronic hepatitis C liver tissue or HCC may be used for the diagnosis and creatment of these diseases. Such genes inhibitors of their expression or activity, and antibodies against the spen products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV84691-ABV84790 are SAGE tags representing the 100 least highly expressed genes out of those genes which are underexpressed in hepatocellular carcinoma compared with chronic hepatitis C liver tissue
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                                                                                                                                                                                                               ABV84695 standard; cDNA; 10 BP
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88.9%;
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Best Local Similarity
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ABUN4695
AC ABUN496
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AC ABUN499
AC ABUNAN
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GGACGCGCT

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RESULT 369 ABV84296

3 GGACTCGCT 11

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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C-induced in human liver tissue.

The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C invertissue or HCC, antibodies against these proteins, and inhibitors of the expression of genes that are overexpressed in chronic hepatitis C liver tissue or HCC. Groups of genes differentially expressed in chronic hepatitis C tissue or HCC. Groups of genes differentially expression or activity, and antibodies against the gene products may be used in the expression or activity, and antibodies against the gene products may be used in the expression or activity, and antibodies against the gene products may be used in the expression or activity of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV94291-ABV84390 are SAGE tags representing the low least highly expressed genes out of those genes which are underexpressed in chronic expressed genes out of those genes which are underexpressed in chronic
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SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss.
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Best Local Similarity 88.5-
8; Conservative
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ID ABV8
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AC ABV8
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DT 12-I
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C -induced human liver tissue.

The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the S'-CATG-3' sequence motif lying nearest to the polyh region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis of liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes there are overexpressed in chronic hepatitis C liver tissue or HCC frowps of genes differentially expressed in chronic hepatitis C tissue or HCC may be used for the diagnosis and chronic hepatitis C tissue or HCC may be used for the diagnosis and creativity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC Sequences Appressed genes out of those genes which are underexpressed in the expressed genes out of those genes with normal liver tissue
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                                                                                                                                                                                                                                                             (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                             Claim 28; Page 19; 139pp; Japanese
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Matches
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The invention relates to SAGE (serial analysis of gen. expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CM) liver tissue or hepatitis C-induced in human liver tissue.

The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the S-CATG-3' sequence motifilying nearest to the collected downstream of the S-CATG-3' sequence motifilying nearest to the polya region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis of liver tissue or HCC, antibodies against these proteins, and inhibitors of hepatitis C liver tissue or HCC. Groups of genes that are overexpressed in Chronic hepatitis C tissue or HCC may be used for the diagnosis and creatment of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV848611-ABV84790 are SAGE tags representing the loo least highly expressed genes out of those genes which are underexpressed in hepatocellular carcinoma compared with chronic hepatitis C liver tissue hepatocellular carcinoma compared with chronic hepatitis C liver tissue ö SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; Gaps Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes. ö 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other; (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN. (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN Claim 46; Page 26; 139pp; Japanese. Human ceruloplasmin SAGE tag #782. ВР 19-JAN-2001; 2001JP-00012328. 19-JAN-2001; 2001JP-00012328 19-JAN-2001; 2001JP-00012328 ABV84972 standard; cDNA; 10 (first entry) Query Match
Best Local Similarity 88.9
Matches 8; Conservative expression pattern; ss 4 GACTCGCTG 12 GACGCGCTG 10 WPI; 2002-631294/68. JP2002209591-A. Homo sapiens 12-DEC-2002 30-JUL-2002. ABV84972; RESULT 372 ABV84972/c ò 원 ô SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss.

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1; Indels

37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02;

Pred. No. 1.6e 0; Mismatches

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                                                                                                     The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis (C (H) liver tissue or hepatitis (C-induced control pepatitis (C (H) liver tissue or hepatitis (C -induced control pepatitis (C -induced) the paparocallular carcinoma (HCC) compared with normal human liver tissue. The SAGE tags of this invention consist of a sequence of 10 mucleotides located downstream of the S -CATG-3 sequence motif lying nearest to the polyh region of the S -CATG-3 sequence motif lying nearest to the polyh region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, groups of genes that are overexpressed in chronic hepatitis C tissue or HCC may be used for the diagnosis and treatment of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences ABV84891-ABV849990 are SAGE tags representing 100 genes which are highly expressed in hepatocellular carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss.
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                                Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 46; Page 26; 139pp; Japanese.
                                                                            Claim 64; Page 31; 139pp; Japanese
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les 8; Conservative
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WPI; 2002-631294/68
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chronic hepatitis C (CH) liver tissue or hepatitis C-induced
hepatocellular carcinoma (HCC) compared with normal human liver tissue.
The SAGE tags of this invention consist of a sequence of 10 nucleotides
located downstream of the 5'-CANG-3' sequence motif lying nearest to the
polya region of cDNAs derived from a variety of genes. These tags serve
to uniquely lidentify each transcript and can thus be used to analyse the
pattern of gene expression in particular cell types. The invention also
relates to proteins encoded by the genes expressed in chronic hepatitis C
liver tissue or HCC. Antibodies against these proteins, and inhibitors of
the expression of groups of genes that are overexpressed in chronic
hepatitis C liver tissue or HCC. Groups of genes differentially expression
c no farronic hepatitis C tissue or HCC may be used for the diagnosis and
treatment of these diseases. Such genes inhibitors of their expression
or activity, and antibodies against the gene products may be used in the
development of drugs to treat chronic hepatitis C and/or HCC. Sequences
ABV84691-ABV84790 are SAGE tags representing the 100 Least highly
expressed genes out of those genes which are underexpressed in
hepatocellular carcinoma compared with chronic hepatitis C liver tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human multiple HCC/CH differentially expressed genes SAGE tag #414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels
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Best Local Similarity 88.9
Matches 8; Conservative
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Gaps

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Indels

Pred. No. 1.6e+02;); Mismatches 1;

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2 CGCTGGCCC

8 CGCTGGCAC 16

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Gaps ;

88.98;

Best Local Similarity 88.9 Matches 8, Conservative

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liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis C liver tissue or HCC. Groups of genes differentially expressed in chronic hepatitis C tissue or HCC may be used for the diagnosis and chromic hepatitis C tissue or HCC may be used for the diagnosis and readment of these diseases. Such genes, inhibitors of thair expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis C and/or HCC. Sequences expressed genes out of those genes which are overexpressed in hepatocellular carcinoma compared with chronic hepatitis C liver tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human Ran GTPase activating protein 1 (RANGAPI) gene located on chromosome 2243.2-43.31, and methods for haplotyping and/or genotyping the RANGAPI gene. The methods of the invention make use of allele-specific oligonucleotides (ASOS) as probes and primers and/or primer-extension oligonucleotides for detecting the RANGAPI gene polymorphisms. The polymorpheotides and screened compounds are useful for treatment of diseases associated with RANGAPI activity, such as cancer and other disorders associated with an irregular cell cycle, AAS19821-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, single nucleotide polymorphism, SNP, RANGAP1,
haplotyping chromosome 22q13.2-q13.31; Ran GTPase activating protein 1,
genotyping; cancer; irregular cell cycle associated disorder; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genotyping human Ran GTPase activating protein 1 gene of individual for determining haplotype of individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide #71 to detect human RANGAP1 gene polymorphisms.
                                                                                                                                                                                                                                                                            37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels
liver tissue or HCC, antibodies against these proteins,
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                                                                                                                                                                                                                                   Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 16; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS19891 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                            Query Match 37.0
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                              11 TGGCACGCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 375
AAS19891
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The invention relates to an isolated polynucleotide comprising a sequence selected from a polymorphic variant of calmodulin 1 (CALMI). The polymorphic variant comprises an CALMI isogene defined by a haplotype selected from haplotypes 1-21 given in the specification. The polymorphisms are useful for studying the biological function of CALMI as the identifying drugs targeting this protein for the treatment of a disorder related to its abnormal expression or function. The polymorphic variants may also be used in screening for the treatment of targeting CALMI to treat a specific condition or disease predicted to be associated with CALMI activity. Steablishing CALMI haplotype or haplotype pair of an individual is useful for improving the efficiency and relability of several steps in the discovery and development of drugs clibability of several steps in the discovery and development of drugs disease and diseases involving defects in calcium-dependent signal transduction. Haplotyping the CALMI gene in an individual is also useful the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with CALMI activity, ASSSS892-AASSG018 represent human CALMI alleje- specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in expressing CALM1 protein for use in screening for candidate drugs to treat diseases related to CALM1 activity such as Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                 SNP;
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                                                                                                                                                             Calmodulin 1; CALM1; human; single nucleotide polymorphism; haplotyping; SCYA3; Alzheimer's disease; drug screening; calcium-dependent signal transduction; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stephens JC;
                                                                                                                        Human CALM1 gene allele-specific oligonucleotide #89.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi JY, Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 14; 82pp; English.
AAS95980 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                          12-APR-2000; 2000US-0196340P.
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                                                                               26-FEB-2002 (first entry)
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                      WO200179218-A2.
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                                           AAS95980;
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DB 1; Length 10

37.0%; Score 7.4;

Query Match

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WPI; 2002-519113/55.
                                                                                                                                                                                                                                                                                                      Bentivegna SC,
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                          05-SEP-2002
                                                                                                                                     Homo sapiens
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AAL39813;
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New genetic variants of smoothened Drosophila homolog (SMOH) gene useful for therapeutic purposes and for expressing SMOH protein useful in identifying drugs to treat basal cell carcinomas.

Sausker EA;

Lee HH,

The invention relates to an isolated polymuclectide comprising a sequence which is a polymorphic variant of a reference sequence for the human emothered Diosophila homologue (SMOH) gene or its fragment, or a polymorphic variant of a reference sequence for a SMOH CDNA or its fragment. A new isolated polypeptide is useful for identifying an association between a trait such as a clinical response to a drug targeting the polypeptide. A new method is useful for identifying an association between a trait such as a clinical response to a drug targeting SMOH and a haplotype or haplotype pair of SMOH gene. The methods have applicability in developing diagnostic tests and therapeutic treatments for basal cell carcinomas (BCCs). The isolated polymucleotide is useful for studying the expression and function of SMOH and expressing SMOH protein for use in screening for candidate drugs to treat diseases related to SMOH activity. The polymorphism and haplotype do treat BCCs, screening for the drugs and reducing bias in clinical trials of the screening for the drugs and reducing bias in clinical trials of the screening for the drugs and reducing bias in clinical trials of the for determining whether an individual has one of the haplotypes or the treat disorders by gene therapy and antisense gene therapy. This continue sequence represents a primer used for detecting human smoothened Drosophila homologue gene polymorphisms of the invention

Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

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0
            Local Similarity 88.5
les 8; Conservative
Query Match
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Gaps

RESULT 378

Cytostatic, polymorphic variant, single nucleotide polymorphism, SMOH, human smoothened Drosophila homologue; basal cell carcinoma; BCC; gene therapy, PCR; primer; ss. SMOH polymorphism detecting primer SEQ ID No 128. Choi JY, Koshy B, Claim 17; Page 16; 179pp; English. (GENA-) GENAISSANCE PHARM INC. AAL39813 standard; DNA; 10 BP. 04-OCT-2001; 2001WO-US031304. 04-OCT-2000; 2000US-0237871P. (first entry)

Score 7.4; DB 1; Length 10; Pred. No. 1.6e+02; 0; Mismatches 1; Indels 37.0%; 7 TCGCTGGCA 15

ACA94531 standard; DNA; 10 BP. ACA94531 ID ACA

(first entry) 18-JUL-2003 DNA tag from human transcript repressed in adenomas/cancers #64.

Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase; macrophage inhibitory cytokine; MIC; RDP; faeces; blood; kidney proximal tubule.

Homo sapiens.

402003022863-A1.

20-MAR-2003.

09-SEP-2002; 2002WO-US028518.

07-SEP-2001; 2001US-0317494P.

(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

Buckhaults P, Kinzler KW, Vogelstein B;

PI; 2003-313220/30.

perecting colorectal cancer in a subject, involves derecting macrophage inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood of the subject.

Disclosure; Page 28; 59pp; English.

The invention relates to detecting macrophage inhibitory cycuckine (MIC) adenoma), comprising: (a) detecting macrophage inhibitory cycuckine (MIC) or renal dispetidase (RDP) in faces or blood of a subject and comparing amount of MIC or RDP detected to that in normal subjects, where an elevated amount of MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP mRNA in the subject is an indicator of CC in control faces of a subject, (c) and indicator of CC in subject, (b) isolating mRNA sample, and comparing the amount of MIC or RDP mRNA in the subject is an indicator of CC in subject, (c) ample to mRNA ample, and comparing the amount of MIC or RDP mRNA ample to amounts of MIC or RDP mRNA sample to amount of MIC or RDP mRNA in normal subjects, where on a blood or faces of a subject or epithelial cells, detecting an mRNA sample to amount of MIC or RDP mRNA in normal subjects, where or cc in the subject; (d) contacting blood or faces of a subject, with an RDP substrate, detecting activity of RDP in the blood or faces by a detection of increased reaction product or decreased RDP substrate, and comparing the amount of activity of RDP in the blood or faces by detection of increased reaction product or decreased RDP substrate, and comparing the amount of activity of RDP in the blood or faces by contact to that in normal subject; where an elevated amount of activity of RDP in the blood or faces of the subject is an indicator of CC in the subject; (e) administering to a subject and antibody which specifically contact to RDP or an inhibitor of RDP, where the antibody or inhibitor is labeled with a moiety which is detectable from outside of the subject and cercased contact a substrate for RDP, the subject and outside of the subject was a product or decreased with the detectable moiety, where increased product or decreased with the detectable moiety, where increased product or decreased with the detectable moiety, where increased product or decreased with the detectable moiety, where increased product or decre

Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other,

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Gaps

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The invention relates to detecting CC (colorectal cancer e.g. colorectal adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC) or renal disperialise (RDP) in faces or blood of a subject and comparing camount of MIC or RDP detected to that in normal subjects, where an elevated amount of MIC or RDP in the subject is an indicator of CC in Subject; (b) isolating mRNA sample from faces of a subject, detecting MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP mRNA in the subject is an indicator of CC in subject; (c) isolating epithelial cells from blood of a subject, isolating an mRNA sample from faces of a subject or RDP mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where an elevated amount of MIC or RDP mRNA in normal subject, with a nelevated amount of MIC or RDP mRNA in the mRNA sample to amounts of MIC or RDP mRNA in normal subject, with a nelevated amount of MIC or RDP mRNA in the mRNA sample to an indicative of CC in the subject, (d) contacting blood or faces of a subject, with a comparing the amount of activity of RDP in the blood or faces by detecting activity of RDP in the blood or faces of the subject to that in normal subjects, where an elevated amount of activity of RDP in the blood or faces of the subject is an indicator of CC in the blood or faces of the subject an antibody or inhibitor is labeled with a moiety which is detectable from outside of the subject and detecting the moiety within the subject but outside the proving to a subject area of localisation of the moiety within the subject but outside the proving to a subject or of subject a substrate for RDP, the substrate being labeled with a substrate for RDP, the substrate being labeled with a substrate for RDP, the substrate being labeled with a substrate for RDP, the substrate being labeled with a substrate for RDP, or o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase; macrophage inhibitory cytokine; MIC; RDP; faeces; blood; kidney proximal tubule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA tag from human transcript repressed in adenomas/cancers #104.
        Length 10;
    Score 7.4; DB 1; Length 10
Pred. No. 1.6e+02;
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        37.0%;
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                                                                                         Conservative
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Query Match
Best Local Similarity
Matches 8; Conserv
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The invention relates to detecting CC (colorectal cancer e.g. colorectal adenoma), comprising: (a) detecting macrophage inhibitory cytckine (MIC) or renal dipeptidase (RDP) in faces or blood of a subject and comparing camount of MIC or RDP detected to that in normal subjects, where an elevated amount of MIC or RDP in the subject is an indicator of CC in subject; (b) isolating mRNA sample from facese of a subject, detecting MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP mRNA in the subject is an indicator of CC in subject; (c) ror RDP mRNA in the subject is an indicator of CC in subject; (c) isolating epithelial cells from blood of a subject; isolating an mRNA sample from faces of a subject or epithelial cells, detecting MIC or RDP mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in che mRNA sample from MIC or RDP mRNA in the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative of CI in the subject; (d) contacting blood or facese of a subject, with an RDP substrate, detecting activity of RDP in the blood or facese by detection of increased reaction product or decreased RDP substrate, and
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detectable moiety, isolating faeces or blood from the subject, and detecting in the faeces or blood RDP reaction product or RDP substrate with the detectable moiety, where increased product or decreased substrate in the faeces or blood indicates CC in the subject. The methods are useful for detecting colorectal cancer in a subject. The present sequence is a DNA tag derived from a human transcript whose expression is repressed in colorectal cancer or colorectal adenoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting colorectal cancer in a subject, involves detecting macrophage inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood of the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase; macrophage inhibitory cytokine; MIC; RDP; faeces; blood; kidney proximal tubule.
                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.6e+02;
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88.9%;
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30-MAY-2002; 2002US-0383805P.
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Best Local Similarity 88...
...a 8; Conservative
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comparing the amount of activity of RDP in blood or faeces of the subject to that in normal subjects, where an elevated amount of activity of RDP in the blood or faeces of the subject is an indicator of CC in the subject; (e) administering to a subject an antibody which specifically binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is labeled with a moiety which is detectable from outside of the subject and area of localisation of the moiety within the subject but outside the proximal tubules of the kidney identifies CC; or (f) administering to a subject a substrate for RDP, the substrate being labeled with a detectable moiety, isolating faeces or blood from the subject, and detectable moiety, where increased product or RDP substrate with the detectable moiety, where increased product or RDP substrate with the detectable moiety, where increased product or RDP substrate of the subject in the faeces or blood indicates CC in the subject. The methods are useful for detecting colorectal cancer in a subject. The present substrate is a DRA tag derived from a human transcript whose expression is
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30-UUL-1999; 99US-01465959
30-UUL-1999; 99US-01461592
23-WAR-2000; 2000US-00515008
20-NOV-2000; 2000US-00716637.
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for their target sequences, as well as enhanced biological activity. The present sequence represents a zinc finger protein DNA target sequence.
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                                                                   Score 7.4; DB 1; Length 10;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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                                             Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
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99US-0126239P.
99US-0146595P.
99US-0146615P.
2000US-00535008.
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                                                        Query Match
Best Local Similarity 86...
8; Conservative
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New gene encoding a protein having ethanolaminephosphate cytidyltransferase activity, useful for treating Zellweger's syndrome, or lipid-related diseases such as cardiovascular diseases and obesity.
                                                                                                                                                                                                                                                                                                     The invention relates to a mouse gene encoding a protein having ethanolaminephosphate cytidyltransferase (ET) activity appearing as ADD71226, a degenerate variant of the ET gene, or a Sequence that hybridises to the complement of the ET gene under stringent conditions. Also included is a promoter of a human ethanolaminephosphate cytidyltransferase gene appearing as ADD71227. The gene and promoter are useful for producing a transgenic animal, and for idertifying, preventing, and treating diseases (by gene therapy) related to inappropriate phosphatidylethanolamine production, e.g. Zellweger's syndrome, or lipid-related diseases such as cardiovascular diseases, atherosclerosis and obesity. The present sequence is a mouse ET gene 3' splice acceptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mammalian model for enhanced wound healing - useful for identifying
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                                                                                                                Poloumienko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ACTCGCTGG 13
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                                                        BAKO/) BAKOVIC M. (POLO/) POLOUMIENKO
                                                                                                                                                       WPI; 2003-844457/78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ACTOTOTOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WIST-) WISTAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-1998;
26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1999
                                                                                                                Bakovic M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heber-Katz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ18867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel monobactam compounds. A compound of the invention has antibacterial activity, and acts as a PBP2a inhibitor. The compounds are used as antibacterial agents. The monobactam compounds restore sensitivity of methicillin resistant Staphylococcus aureus to lactam antibiotic by targeting the molecular mechanism of resistance. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse, ethenolaminephosphate cytidilyl transferase, ET; ds;
splice acceptor site; antilipemic; cardiant; anorectic;
phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;
cardiovascular disease; atherosclerosis; obesity.
                                                                                                                                                                      ss; monobactam; antibacterial; PBP2a; inhibitor;
methicillin resistant Staphylococcus aureus; MRSA; lactam antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compounds used as antibacterial agents against e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse ET gene 3' aplice acceptor site from intron 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                   Monobactam related tethered diene SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dewey T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methicillin resistant Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; SEQ ID NO 22; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nieuwlandt
              ADC17772 standard; DNA; 10 BP.
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ID ADD71264 standard; DNA; 10 BP
XX
XX
XX
XX
ADD71264;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mouse ET gene 3' splice accep
XW
Mouse; ethenolaminephosphate
XW
Splice acceptor site; antilip
XW
Splice acceptor site; antilip
XW
ADD71264;
XX
W
US2003194795-A1.
XX
PD 16-OCT-2003.
XX
PF 21-MAR-2002; 2002US-00101957.
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                                                                                                                                                                                                                                                                                                                                                .8-DEC-2002; 2002WO-US040739
                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2001; 2001US-0340255P
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Ouery Match
Best Local Similarity 88.7%,
Best Local Similarity 88.7%,
                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                             (INVE-) INVENUX INC
                                                                                                                                                                                                                                                                      WO2003051314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New monobactam
                                                                                           18-DEC-2003
                                                                                                                                                                                                                                                                                                           26-JUN-2003
                                                                                                                                                                                                                              Synthetic
                                                      ADC17772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eaton B,
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RESULT 384

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Gaps

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This invention describes a novel non-WRL healer mouse (W) having at least one quantitative trait locus selected from those given in the specification, exhibiting an enhanced healing response to a wound compared to mice (W) without the locus. The invention describes a novel method of identifying agene involved in enhanced wound healing by identifying DNA microsatellite markers which and identifying microsatellite markers which sergegate with enhanced wound healing in progeny of the mice, where a chromosomal locus containing at least one enhanced wound healing gene is identified. A method of treating a wound; a mammal is also disclosed. The new methods are useful for treating wounds, especially central and periods function after nerve injury in a mammal. (M) is useful as a mammalian model of enhanced wound healing, useful for identifying genes and per products involved in enhanced wound healing, and to provide methods for wound healing. Asialogic represent murine SAGE tags from C57BL/6 and MRL mice which are used to illustrate the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.0%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 1.7e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11 BP; 2 A; 6 C; 2 G; 1 T; 0 U; 0 Other;
                                                                  Claim 13; Page 71; 136pp; English
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98US-0097937P.
98US-0102051P.
enhanced wound healing genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
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26-AUG-1998;
28-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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AZISTONIA AZ
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This invention describes a novel non-MRL healer mouse (M) having at least one quantitative trait locus selected from those given in the

Claim 13; Page 57; 136pp; English.

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specification, exhibiting an enhanced healing response to a wound compared to mice (m) without the locus. The invention describes a novel method of identifying a gene involved in enhanced wound healing by identifying a gene involved in enhanced wound healing by identifying DNA microsatellite markers which from non-healer mice and identifying microsatellite markers which sepregate with enhanced wound healing in progeny of the mice, where a chromosomal locus containing at least one enhanced wound healing gene is identified. A method of treating a wound in a mammal is also disclosed. The new methods are useful for treating wounds, especially central and peripheral nerve wound. The methods of the invention are useful for restoring function after nerve injury in a mammal. (M) is useful as a mammalian model of enhanced wound healing, useful for identifying genes methods for wound healing. AAZI8691-Z19036 represent murine SAGE tags from C57BL/6 and MRL mice which are used to illustrate the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for, (A) comprises protein or mRNAs or their fragments, (M1) is useful for; identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 7.4; DB 1; Length 11; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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Best Local Similarity 88.9%;
Matches 8; Conservative
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RESULT 388

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Conradt M, Hofmann K;
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                                                                                                                                                                                               20-DEC-2001; 2001WO-EP015178.
                                                                                                                                                                                                                           03-JAN-2001; 2001DE-01000121
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                           (first entry)
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Best Local Similarity 86.2
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                                                                                                               Homo sapiens
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                            10-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                     37.0%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 1.7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.0%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 1.7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                Human skin stress/ageing related EST SEQ ID NO 939
          Sequence 11 BP; 0 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
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expression.
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ABQ86321 ID ABQ XX

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The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for. (A) comprises protein or mRNAM or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; and identifying or determining the effects of skin ageing and/or stress; and identifying or determining the effects of sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQB6246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and aging, useful e.g. in its, based or differential
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                                                                                       Human; skin ageing; skin stress; BST; expressed sequence tag;
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Human skin stress/ageing related EST SEQ ID NO 76.
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                                                                                                                                                                                                                                              Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                            Hofmann
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88.9%;
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                                                                                                                     Petersohn D,
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or ichthyosis; atopic dermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Best Local Similarity 99.9%;
Matches 8; Conservative 0
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ABV69501 standard; cDNA; 11
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                                ABV69501;
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                                  Length 11;
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Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
                                7.4; DB 1;
No. 1.7e+02;
                                Score 7.4; DB Pred. No. 1.7e 0; Mismatches
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88.9%;
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RESULT 394 ABV69501

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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or ichthyosis; specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhaz; lupus arythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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neurodermatitis;
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhae.
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatit:
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn; psoriasis; scleroderma;
                                                                                                                                                                                                                     In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of skin. The present sequence is that of a human expressed sequence tag
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                                                                             20-DEC-2001; 2001WO-EP015179.
                                                                                                           03-JAN-2001; 2001DE-01000127.
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Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                            The invention relates to in vitro identification (W1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psociatis scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinom; or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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(MI) is useful for identifying genes involved in skin homeostasis; to
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                               In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Pred. No. 1.7e+02;
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                                                                                                    Claim 24; Page 269; 1345pp; German.
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WPI; 2002-590638/63
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                                                                   e.g. skin cancer.
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
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Query Match
Best Local Similarity 88.5
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixtune of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus crythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BSI) of the invention
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                                                                                                        ABV68885 standard; cDNA; 11
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37.0%; Score 7.4; DB 1; Length 11; larity 88.9%; Pred. No. 1.7e+02; Conservative 0; Mismatches 1; Indels

Local Similarity nes 8; Conserv

Best Loc Matches

Query Match

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

Disclosure; Page 42; 1345pp; German.

e.g. skin cancer.

Hofmann K;

Conradt

Petersohn D,

(HENK) HENKEL KGAA

WPI; 2002-590638/63

20-DEC-2001; 2001WO-EP015179 03-JAN-2001; 2001DE-01000127

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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
     Human skin EST 3266
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; pscriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; ichthyosis; melanoma; basal cell carcinoma; and carcinoma; or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; icthhyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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88.9%;
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hes 8; Conservative
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Score 7.4; DB 1; Length 11; Pred. No. 1.7e+02; 0; Mismatches 1; Indels

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3 GGCACACAC 11

37.0%; 88.9%;

Sequence 11 BP; 3 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

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In vitro identification of skin-expressed genes, useful for determining homeostagis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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RESULT 402
ABV63636/c
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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

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ABV62831 standard; cDNA; 11

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11 ACTGGCTGG

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(first entry)

21-OCT-2002

ABV62831;

Human skin EST 617

WO200253774-A2

11-JUL-2002

Homo sapiens

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis, acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
                                                    The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from Skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agant (A) that maintains or promotes skin homeostasis or that can be used for treating skin disordders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                    Disclosure; Page 64; 1345pp; German
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ID ABV67898 standard; cDNA; 11 BP.
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88.9%; Pred. No. 1.7e+02;
ative 0; Mismatches 1; Inde's
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                                              Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
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     skin. The present sequence (EST) of the invention
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ABV69088;

RESULT 405

11-JUL-2002.

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for traiting skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermaitis; acne; seborrhes; lupus erythematosus; rosaces, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss
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Matches
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                                                                                                                                                                                                                                 Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                               ABV69088 standard; cDNA; 11 BP.
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Best Local Similarity 88.2
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ABV65801;

ABV65801
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DE Hume
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RESULT 406

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Gaps

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Conradt M,
                              WPI; 2002-590638/63
Petersohn D,
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Hofmann K;

Disclosure; Page 171; 1345pp; German

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to the can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborntea; lupus expthematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Gaps ô 37.0%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 1.7e+02; 1; Indels 0; Mismatches 8; Conservative Query Match Best Local Similarity Matches

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ABV71057 standard; cDNA; 11 BP ABV71057;

(first entry) 21-OCT-2002

Human skin EST 8843

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

sapiens

WO200253774-A2

11-JUL-2002

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA

Ķ Hofmann Petersohn D, Conradt M,

WPI; 2002-590638/63

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against g. skin cancer.

Claim 24; Page 284; 1345pp; German

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically

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encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (Ml) is useful for identifying genes involved in skin momeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis, soleroderma, ichthyosis, atopic dermatitis, acne, sebornhea, lupus erythematosus; rosacea, melanoma, basal cell cardinoma, and cardinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Gaps ö 37.0%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 1.7e+02; tive 0; Mismatches 1; Indels Conservative Local Similarity nes 8; Conserv Query Match Matches

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12 GGCACGCAC 20 GGCACTCAC 1 8 엄

ABV67744 standard; cDNA; 11 ABV67744;

BP.

21-OCT-2002

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Human skin EST 5530

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens

WO200253774-A2

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA

Hofmann K; Conradt M, Petersohn D,

WPI; 2002-590638/63

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 177; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin immeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag ABV67744/C

IX ABV67744/C

XX ABV6774

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Seguence 11 BP; 1 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

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ò g ABV62437;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                                Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE; neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
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88.9%;
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Best Local Similarity 88.5.
Best Local 8; Conservative
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                                                                            Human skin EST 997
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                                      21-OCT-2002
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ABV63211;
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immunosuppressive, antiinflammatory, cytostatic; SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Score 7.4; DB 1; Length 11; Pred. No. 1.7e+02; Mismatches 1; Indels
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88.9%;
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37.0%;
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Best Local Similarity 88.5
Matches 8, Conservative
                                        Conservative
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Best Local Similarity
Matches 8; Conserv
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RESULT 411
ABV63211
ID ABV632:

Hofmann K;

20-DEC-2001; 2001WO-EP015179.

11-JUL-2002

Vogelstein

Kinzler KW,

St Croix B,

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriatis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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                                                                                                                                                                                                      In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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SNINGO UNIV (OLYU)

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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABB92075-ABB921141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL92041 and ABB92143-ABB92191; normal endothelial markers (NEM) ABL92041, and pan-endothelial markers (NEM) ABL92041, and pan-endothelial markers oligonucleotide sequence is that of an oligonucleotide marker useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53 protein, pGL3 luciferase reporter vector, luc+, transcription factor, cell cycle control; DNA damage repair; pGL3 basic vector; apoptosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining the p53 status of a sample, useful for assaying for mimetics or antagonists of p53, or for the presence of DNA damage, comprises determining whether p53 binds to the pGL3 vector in a sample containing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patent discloses methods for determining the p53 status of a sample
                                                                      An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tunor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pGL3 basic vector CCCGGG motif 5' flanking DNA.
                                                                                                                                                 Example 4; Page 324; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 12; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD27543 standard; DNA; 11 BP
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which comprise providing a sample containing a pGL3 luciferase reporter vector and determining whether p53 binds to the pGL3 vector. p53 is a transcription factor that regulates many genes including those associated with call cycle control, apoptoals and DNA damage repair. pGL3 reporter vectors contain a modified firefly luciferase cDNA designated luc+. p53 protein binds to pGL3-basic vector and causes luciferase expression. The method is useful for determining the p53 status of a sample. It is also useful for assaying for mimetics or antagonists of p53 and for assaying for the method of modifying pGL3 vector which involves deletion or relates to a method of modifying pGL3 vector which involves deletion or alteration of a CCCGGG motif of the pGL3 vector and/or deleting or alterating a sequence incorporating the CCCGGG motif. The nucleic acid having a sequence incorporating the CCCGGG motif is useful for conferring promoter activity or p53-responsiveness on a nucleic acid motificy. The present DNA sequence is pGL3 basic vector CCCGGG motif for conferring breamth of a polypeptide of interest or in assays for p53 transcriptional activity. The present DNA sequence is pGL3 basic vector CCCGGG motif for conferr activity when also also motified motifit to conferr promoter activity.
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Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

ö Gaps o; 37.0%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 1.7e+02; rative 0; Mismatches 1; Indels Query Match Best Local Similarity 88.7 Lac 8; Conservative

10 CTGGCACGC 18

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11 Db ABX71836 standard; DNA; 11 BP.

ABX71836;

12-MAR-2003 (first entry)

DNA tag used to identify human gene encoding PEM 9.

Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; necangiogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.

Homo sapiens

WO200283874-A2

24-OCT-2002

10-APR-2002; 2002WO-US008253

11-APR-2001; 2001US-0282850P. 06-FEB-2002; 2002US-0354262P.

UNIO (OLYU)

Vogelstein B; Kinzler KW, Carson-Walter E, St Croix B,

WPI; 2003-093016/08,

New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

Disclosure; Page 89; 374pp; English.

The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in

normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (WEM) genes are indothelial marker (WEM) genes are identified in human ECs. The human EC marker proteins and the polymucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycyptic lidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoanglogenesis or tumour anglogenesis, for inducing an immune response to tumour endothelial calls in a patient, or for identifying candidate drugs for treating tumours. ABX71828-ABX71899 represent DNA tags for human PEM, TEM or NEM genes 88666666666888888

Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Gaps .. 0 37.0%; Score 7.4; DB 1; Length 11; 88.9%; Pred. No. 1.7e+02; ative 0; Mismatches 1; Ind@ls 8; Conservative Best Local Similarity Matches 8; Conserv Query Match

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15 7 TCGCTGGCA ð 8, 2004, 12:25:35 Search completed: June Job time: 2 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- nucleic search, using sw model OM nucleic

8, 2004, 12:21:50 ; Search time 0.001 Seconds (without alignments) 141.480 Million cell updates/sec June Run on:

US-10-003-919-21 20 1 ATGGACTCGCTGGCACGCAC 20 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

634 Total number of hits satisfying chosen parameters:

317 seqs, 3537 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 318 summaries

rgedb:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	ACCESSION: AX292886 ACCESSION: AX211959 ACCESSION: AX098804 ACCESSION: AX039021 ACCESSION: AX339221 ACCESSION: AX33021 ACCESSION: AX350138 ACCESSION: AX260358 ACCESSION: AX260358 ACCESSION: AX260358 ACCESSION: AX260358	ACCESSION; AR286771 ACCESSION; AR286771 ACCESSION; AK624655 ACCESSION; AK622076 ACCESSION; ED005994 ACCESSION; ED005994 ACCESSION; E14044 ACCESSION; E14044 ACCESSION; E14044 ACCESSION; E14041 ACCESSION; AR286741 ACCESSION; AK696541 ACCESSION; AK696541 ACCESSION; AK696541 ACCESSION; AK69696
SUMMARIES	AX292886 AR211959 AR091804 AR074734 AX39221 AX3920138 AX360138 AX268358 AR228418 AR268358	AR285771 AK397762 AK32465 AK32076 BD005894 AR175758 B13070 B13070 B1464 AR183001 AX826741 AX826741 AX82149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62149 AX62140
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LOCUS DEFINITION ACCESSION VERSION	AX292886 20 bp DNA linear PAT TON Sequence 4648 from Patent WO0179548. ON AX292886 AX292886.1 GI:17054569	21-NOV-2001
KEYWORDS SOURCE ORGANISM	Σ	
REFERENCE AUTHORS TITLE JOURNAL FEATURES	Barany, Method Beguence Patent: CORNELL	nucleic acid
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cy an	6 CTCGCTGGCACCCC 20 	
RESULT 2 AR211959/C LOCUS DEFINITION ACCESSION VERSION XEXWORDS		. 20-JUN-2002
SOURCE ORGANISM REFERENCE ATTHORS TITLE JOURNAL FEATURES GOURCE	Unknown. M Unknown. Unclassified. 1 (bases 1 t Ward, D.T. and Antisense mod Patent: US 63 Patent: US 63 Ce 1	
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Qy Dp	2 TGGACTCGCTGGCACGCA 19 	
RESULT 3 AR098804/c LOCUS DEFINITION ACCESSION VERSION	3 4/c AR098804 18 bp DNA linear PAT ION Sequence 59 from patent US 6077672. ON AR098804 GI:12808570	14-FEB-2001
RETWORDS SOURCE ORGANISM REFERRICE AUTHORS TITLE JOURNAL FEATURES	Unknown. ISM Unknown. Unclassified. Unclassified. CE 1 (bases 1 to 18) RS Monia,B.P. and Cowsert, L.M. Antisense modulation of TRADD expression A. Patent: Use 5077672-A 59 20-UN-2000; Location/Qualifiers	

source

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SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL FEATURES

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PAT 17-AUG-2003

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Unknown.
Unclassified.
1 (bases 1 to 16)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown.
Unclassified.
Unclassified.
Unclassified.
Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Vogelstein,B., Kinzler, K.W., Zhang,L. and Chou,W.
Gene expression profiles in normal and cancer cells
Patent: US 6331352-A 637 25-DEC-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Length 12;
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Immunisation against Chlamydia pneumoniae
Patent: Wo 0202606-A 661 10-JAN-2002;
Chiron S.p.A. (IT)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="Primer tail"
                                             DNA
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Seguence 637 from patent US 6333152.
AR180569
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                                                                                                                                                                                                                                                                                                                                                                          Score 10.4; D
Pred. No. 26;
0; Mismatches
                                           AX350138 12 bp 1
Sequence 661 from Patent WO0202606.
AX350138
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                            AX350138.1 GI:18615816
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                                                                                                                                                                                                                                                                                                                                                                        ch 52.0%;
1 Similarity 91.7%;
11, Conservative (
                                                                                                                            synthetic construct
synthetic construct
artificial sequences.
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Matches 11; Conservative
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Matches 11; Conserv
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            RESULT 6
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AR328418/C
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AR180569
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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1 (bases 1 to 17)

Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic polymorphisms
Patent: US 5955276-A 31 21-SBP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.0%; Score 11; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 17; Matches 11; Conservative 0; Mismatches 0; Indels
                                                               Length 18,
                                                                                                                                                                                                                                               linear
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                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches
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Sequence 31 from patent US 5955276.
AR074734
AR074734.1 GI:10001487
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1. .18
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Sequence 15 from Patent WC0196602.
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Mus sp.
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AX339221/c
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Location/Qualifiers
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                            15 ArdGradcacacióck 1
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Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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Unknown.
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AR285771
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Patent: WO 0175127-A 7 11-OCT-2001;
Ingenium Pharmaceuticals AG (DE)
Location/Qualifiers
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related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 5820 20-MAY-2003;
Location/Qualifiers
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1 (bases 1 to 15)

1 (bases 1 to 15)

Van Mellaert, H., Botterman, J., Van Rie, J. and Joos, H.

Recombinant plant expressing non-competitively binding insecticidal crystal proteins

Insecticidal crystal proteins

Patent: US 6172281-A 2 09-JAN-2001,

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%; Score 10.4; DB 1; Length 16;
Larity 91.7%; Pred. No. 37;
Conservative 0; Mismatches 1; Indels
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                                                                                                    DB 1; Length 16;
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/note="Beschreibung der kunstlichen
Sequenz:Restriktionsschnittstelle Sfi B"
                                                                                                  Score 10.4; DE
Pred. No. 37;
0; Mismatches
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Best Local Similarity 80.0%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches

    .15
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                                            1 . 16
/organism="unknown"
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Sequence 2 from patent US 6172281
AR125055
AR125055.1 GI:14110449
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Sequence 7 from Patent WO0175127.
AX268358 AX268358.1 GI:16541576
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synthetic construct
artificial sequences.
                                                                                                  Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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Matches 11; Conserv
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AX268358/c
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PAT 21-FEB-2003
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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1 (bases 1 to 15)
Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
Oligoribonucleotides with enzymatic activity
Patent: US 6617438-A 143 09-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.0%; Score 10.2; DB 1; Length 15; 80.0%; Pred. No. 39; ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   51.0%; Score 10.2; DB 1; Length 15; 80.0%; Pred. No. 39; 1.1ve 0; Mismatches 3; Indels
                                                                                                                                                                                                        Deigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Sweedler, D. and Zinnen, S. Synthetic ribonucleic acids with RNAse activity Patent: US 6528640-A 143 04-MAR-2003; Location/Qualifiers
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AR285771
Sequence 143 from patent US 6528640.
AR285771
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Sequence 143 from patent US 6617438.
AR397762
AR397762.1 GI:40135008
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AR175758
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                              ch 50.0%; Score 10; DB 1; Length 11; I Similarity 100.0%; Pred. No. 29; 10; Conservative 0; Mismatches 0; Indels
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OS Unidentified

PN 17 2001501825-A/105

PD 13-F3B-2001

PF 03-0CT-1997 JP 1998517095

PR 04-0CT-1996 DK 1096/96,18-OCT-1996 DK

O5-MAY-1997 DK 0512/97
                          Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 1696 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unidentified
unclassified.
1 (bases 1 to 15)
Stender, H., Lund, K. and Mollerup, T.A.
Novel probes for the detection of Mycobacteria
Patent: JP 2001501825-A 105 13-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostaais of the skin
Petent: WO 02053774-A 9118 11-UTL-2002,
Henkel Kommanditgesellschaft auf Aktien (DE)
                                                                                                                                                                                                                                                                                                                                                     AX632076
Sequence 9118 from Patent W002053774.
AX632076.
AX632076.1 GI:28467691
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JP 2001501825-A/105.
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AX632076
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PAT 27-APR-1998
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HENRIK STENDER, KAARE LUND, TINA ANDRESEN MOLLERUP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Universal to 15)
Nishimura, O., Suenaga, M., Ohmae, H. and Tsuji, S. Method for removing N-terminal methionine
Patent: US 6309959-A 3 30-OCT-2001;
Location/Qualifiers
                                                                                /organism='Unidentified'
Location/Qualifiers
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          DNA
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Pred. No. 48;
0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 3 from patent US 6309859.
AR175758
                                                                                                               1. .15
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
PI HENRIK STENDER, KAARE LU
C1201/68, COTM14/00
CC Strandedness: Single;
CC Topology: Linear;
FT Key Locatio:
FT Source 1.15
FT Source /organi:
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Matches 11; Conservative
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Jr 1998072489-A/3

17-MAR-1998

13-JUN-1997 JP 1997156777

14-JUN-1996 JP 96P 154634

NISHIMURA TADASHI, SUENAGA MASATO, OMAE HIROAKI, TSUJI SHINJI

COTKI/12/CLANIS/09,C12P21/02,C12P21/02,(C12P21/02,C12R1:19);

Strandedness: Single;

topology: Linear;

hypothetical: No;
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Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 15)
1 vocation, W. Granggen, J., Stinchcomb, D. and Escobedo, J.
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 8489 12-FEB-2002;
Location/Qualifiers
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Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels
           E15462.1 GI:5710145
Unidentified
SM unidentified
unclassified.

1 (bases 1 to 15)
Nishimura,T., Suenaga,M., Omae,H. and Tsuji,S.
REMOVAL OF N-TERMINAL METHONINE
Patent: JP 1998072489-A 3 17-MAR-1998;
CA MAKEDA CHEM IND LTD
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Chase 1 to 15)

Chase 1 to 15)

E14044.1 GI:5708727

E14044.1 GI:5708727

E25093-A/3.

E3600 Mac H., Suenaga, M. and Nishimura, T.

E2500 Mac H. 1997 E62093-A/3 07-0CT-1997;

E2500 Mac H. 1997 E62093-A/3

E2500 Mac H. 1997 E62093-A/3

E2500 Mac H. 1996 Mac H. 1996 Mac H. 1997;

E2500 Mac H. 1996 
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/organism='Artificial sequences'
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/organism='Artificial sequences'.
Location/Qualifiers
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    15. '15. 'organism="unidentified"
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topology: Linear;
hypothetical: No;
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                                                                                             (bases 1 to 15)

Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
McNatyden, Tor the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 4143 20-MAY-2003;
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1 (bases 1 to 15)

Ito,T., Tanaka,Y. and Kondo,M.
Method for production of recombinant protein
Methon for Droduction of recombinant protein
Patent: WO 0208417-A 70 31-JAN-2002;
TAXEDA CHEMICAL INDUSTRIES LTD,TAKASHI ITO,YOKO TANAKA, MITSUYO
KONDO
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recombinant protein.
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/db_xref="teaxon:32630"
/note="primer"
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 Sequence 4143 from patent US 6566127.
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/mol_type="unassigned RNA"
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WO 0208417-A/70.
synthetic construct
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AR326741.1 GI:33712549
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organism='Artificial Sequence'
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larity 84.6%; Pred. No. 48;
Conservative 0; Mismatches 2; Indels
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Method for production of recombinant protein.
BD176038
Artificial Sequence
%0 0208417-A/70
31-JAN-2005
25-JUL-2001 W0 2001JP006392
25-JUL-2000 JP 00P 229064
TAKASHI 1TO, YOKO TANAKA, MITSUYO KONDO
C12N15/10, C12N1/21, C12P21/02, C12Q1/02
Synthetic DNA
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    .15
    ^organism="synthetic construct"
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JP 2002272481-A/70.
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unidentified
unclassified.
1 (bases 1 to 12)
Fesce,R. and Consalez,G.
METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
Patent: WO 9815521-A 80 02-APR-1998;
FESCE RICCARDO (IT)
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 1; Indels
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

    .11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sequence 80 from Patent WO9813521.
A71521
A71521.1 GI:4775133
 AX624728.1 GI:28452669
                                  Homo sapiens (human)
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Location/Qualifiers
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DP 2002509733-A/34.

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47.0%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels
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Unclassified,
1 (bases 1 to 14)
Ruffner,D.E., Pierce,M.L. and Chen,Z.
Directed antisense libraries
Patent: US 6586180-A 34 01-JUL-2003;
Location/Qualifiers

    12
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Sequence 34 from patent US 6586180.
AR349598.1 GI:33750396
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    .14
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BD225400
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PAT 17-JUL-2003

linear

10 bp DNA Preparation and use of superior vaccines. BD239954

GI:33049724

BD239954.1

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/db_xref="taxon:32644"

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19-UUN-1998 US 60(090041,19-UUN-1998 US 60(089853 PR 19-UUN-1998 US 60(089997,19-UUN-1998 US 60(08997) PR 19-UUN-1998 US 60(08997,19-UUN-1998 US 60(08997) PR 19-UUN-1998 US 60(08997) PR 60(089997,19-UUN-1998 US 60(08997) PR 19-UUN-1998 US 60(08997) PR 60(08997,19-UUN-1998 US 60(08997) PR 19-UUN-1998 US 60(08997) PR 
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(Dases 1 to 10)

Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 833 15-OCT-2002;
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Location/Qualifiers
47.0%; Score 9.4; DB 1; Length 14; 90.9%; Pred. No. 55; tive 0; Mismatches 1; Indels
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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Query Match
Best Local Similarity
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C12N1/19,
C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamala; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10)
1 (bases 1 to 10)
2 (bases 1 to 10)
2 (bases 1 to 10)
3 (bases 1 to 10)
4 (bases 1 to 10)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 0; Indels
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Patent: WO 0138577-A 1189 31-MAY-2001;
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G01N37/00,
PC C12N15/00, C12N15/00
CC Preparation and use of superior vaccines
CC Preparation and Location/Qualifiers
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AX153274
AX153274.1 GI:14534925
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
JP 2002534056-A/1372.
Homo sapiens (human)
Homo sapiens
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/mol_type="unassigned DNA"
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Sequence 4 from patent US 6136568.
AR135802. GI:14476474
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Sequence 3 from patent US 6136568.
AR135801 GI:14476473
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    11 TGGCACGCA 19
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Unknown.
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AR135802
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 0; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 1654 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2828 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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100.0%; Pred. No. 51;
iive 0; Mismatches
                                                                                               h 45.0%; Score 9; DB 1; Similarity 100.0%; Pred. No. 46; 9; Conservative 0; Mismatches
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Sequence 2828 from Patent WO02053774.
                              1. .10
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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The Johns Hopkins University (US)
Location/Qualifiers
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Homo sapiens
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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AX625787
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AX624613
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PAT 21-FEB-2003
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                                                                                                Homo sapiens (human)
Homo sapiens
Eukaryotė, metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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1 (Dases 1 to 12)

Hiatt,A.C. and Rose,F.D.
De novo polynucleotide synthesis using rolling templates
Patent: US 6136568-A 3 24-OCT-2000;
Location/Qualifiers
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                                                                                                                                                                                              Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 9076 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches
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Sequence 9076 from Patent WO02053774.
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RESULT 41
AR362035/c
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AR362037/c
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                        RESULT 40
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Unclassified.

1 (bases 1 to 12)

Hiatt, A.C. and Rose, F.D.
De novo polynoleotide synthesis using rolling templates
Patent: US 6136568-A 4 24-OCT-2000;
Location/Qualifiers
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1 (Dases 1 to 13)
MCGall,M.J., Hendry,P. and Lockett,T.
Optimized minizymes and miniribozymes and uses thereof
Patent: US 601648-A 44 14-DEC-1999;
Location/Qualifiers
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vative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches
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Hendry, P. and McCall, M.J.
Asymmetric harmerbased ribozymes
Patent: US 6238917-A 14 29-MAY-2001;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches
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Sequence 44 from patent US 6001648.
AR094449
AR094449.1 GI:10021381
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Best Local Similarity 100.
Matches 9; Conservative
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TGGACTCGC 1
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AR154534/c
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AR094449/c
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1 (bases 1 to 13)
Cronin,Mr., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A.,
Cronin,Mr., Miyada,C.G., Lobban,P.E., Morris,M.S. and
Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and
Sheldon,E.L.
Sheldon,E.L.
Arrays of nucleic acid probes for analyzing biotransformation genes
and methods of using the same
and methods of using the same
Patent: US 6309823-A 81 30-OCT-2001;
Location/Qualifiers
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monolayers
Patent: US 6600026-A 28 29-JUL-2003;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches
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Sequence 30 from patent US 6600026.
AR362037
13 bp 1
Sequence 81 from patent US 6309823.
AR175358
AR175358.1 GI:17916657
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Sequence 28 from patent US 6600026.
AR362035
AR362035.1 GI:33770186
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches

    .13
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    /mol_type="unassigned DNA"

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/mol_type="genomic DNA"
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Unclassified.
1 (bases 1 to 13)
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Yu, C.
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PAT 17-AUG-2003

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Yu,C.
Electronic methods for the detection of analytes utilizing monolayers
Patent: US 660026-A 42 28-JUL-2003,
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches
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45.0%; Score 9; DB 1;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches
                                                                13 bp I Sequence 42 from patent US 6600026. AR362049. GI:33770200
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Patent: US 6600026-A 44 29-JUL-2003;
Location/Qualifiers
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Sequence 44 from patent US 6600026.
AR362051
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Sequence 45 from Patent W00106016.
AX078151 41:13157896
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AX078151/c
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AR362049/c
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AR362051/c
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Yu,C.
Electronic methods for the detection of analytes utilizing monolayers
Patent: US 6600026-A 30 29-JUL-2003;
Location/Qualifiers
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Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches
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Patent: US 6600026-A 34 29-JUL-2003;
Location/Qualifiers
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Sequence 36 from patent US 6600026.
AR362043
AR362043.1 GI:33770194
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Patent: US 6600026-A 36 29-JUL-2003;
Location/Qualifiers
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Sequence 34 from patent US 6600026.
AR362041
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AR362041/c
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AR362043/c
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PAT 17-AUG-2003

PAT 22-FEB-2001

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PAT 22-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                         Amplification of nucleic acids with electronic detection Patent: WO 0106016-A 53 25-JAN-2001, Clinical Micro Sensors, Inc. (US) Location/Qualifiers
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Matches 9; Conservative 0; Mismatches 0; Indels
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/note="synthetic."
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/mol_type="unassigned DNA"
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/note="synthetic."
Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches
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Sequence 59 from Patent W00106016.
AX078165
AX078165.1 GI:13157910
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Sequence 53 from Patent W00106016.
AX078159 GI:13157904
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AX078167/c
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AX078159/c
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AX078165/c
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 Amplification of nucleic acids with electronic detection Patent: WO 0106016.4 45 25-JAN-2001; Clinical Micro Sensors. Inc. (US) Location/Qualifiers
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Sequence 51 from Patent WO0106016.
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Sequence 47 from Patent WO0106016.
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Sequence 61 from Patent WO0106016.
AX078167
                         AX078167.1 GI:13157912
                                            synthetic construct
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Best Local Similarity 100.
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BD20805/c
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103 B1209911.1

103 B1209911.1

104 B1209911.1

105 B1209911.1

107 B120911.1

                                                                                          BD209807.1 GI:33019577

S BD209807.1 GI:33019577

S Synthetic construct

synthetic construct

artificial sequences.

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S Bamdad.c and Yu.C.

Blectronic detection of nucleic acids using monolayers

LOINITCAL MICRO SENSORS INC

CLINITCAL MICRO SENSORS INC

OS Artificial Sequence

PN 12 2002513592-A47

PD 14-MAY-2002

PF 27-JAN.1999 UP 2000547270

PR 06-MAY-1998 US 60/084425,06-MAY-1998 US 60/084509 PR

17-AGG-1998 US 09/135183

PI CYNTHIA BAMDAD.CHANGYUN YU

PC C1201/68,C07P17/00,C07F19/00,C12N15/09,C12P19/34,G01N27/327,

PC G01N27/416,

PC C1201/68,C07P17/00,G01N27/30,G01N27/46

CC Description of Artificial Sequence: synthetic FH Key Location/Qualifiers

Location/Qualifiers

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RESULT 56 BD209813/c LOCUS

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OS Artificial Sequence
PN 472-202
PD 14-MAY-202
PP 27-JAN-1999 JP 2000547270
PR 66-MAY-1998 US 60/084509 PR 17-JAUG-1998 US 60/084509 PR 17-JAUG-1998 US 60/08425,06-MAY-1998 US 09/135183
PI CYNTHIA BAMDAD, CHANGYUN YU
PC G1201/68, COPF17/00, COPF19/00, C12N15/09, C12P19/34, G01N27/327, PC G01N33/53, C12N15/00, G01N27/30, G01N27/46
PC Description of Artificial Sequence: synthetic FH Key Location/Qualifiers 1. 13
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Beddad.c. and Yu.C.

Electronic detection of nucleic acids using monolayers

Louincal Micro Sensors Inc

SA Artificial Sequence
N 2 2002513592-A61

PD 14-MAY-2002

PP 27-JAN-1999 UP 2000547270

PR 06-MAY-1998 US 60/084425,06-MAY-1998 US 60/084509 PR

I7-Aug-1998 US 09/135183

PC CI201/68,CO7P17/00,CO7F19/00,CI2NIS/09,CI2P19/34,GOINZ7/327,

PC GOINZ3/44,

PC GOINZ3/53,CI2NIS/00,GOINZ7/30,GOINZ7/46

CC Description of Artificial Sequence: synthetic FH Key Location/Qualifiers

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Electronic detection of nucleic acids using monolayers.
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|db_xref="taxon:32630"

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CI2Q1/68, COTF11/00, CO7F19/00, CI2N15/09, CI2P19/34, GOIN27/327,
GOIN27/416,
GOIN37/53, CI2N15/00, GOIN27/30, GOIN27/46
Description of Artificial Sequence: synthetic FH Rey
Location/Qualificial 1: .13
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UP 2002513592-A/53.
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PR 06-MAY-1998 US 60/084425,06-MAY-1998 US 17-AUG-1998 US 09/135183
PI CYNTHIA BAMDAD,CHANGYUN YU
PC C1201/68,C07F17/00,C07F19/00,C12N15/09,C12P
PC G01N33/53,C12N15/00,G01N27/30,G01N27/46
CC Description of Artificial Sequence: synthet
              1. .13
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/db_xref="taxon:32630"

    .13
    ^ organism="synthetic construct"
    /mol type="genomic DNA"
    /db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                   45.0%; Score 9; DB 1;
100.0%; Pred. No. 63;
ative 0; Mismatches
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PP 2002513592-A/59.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 13)
Bamdad,C. and Yu,C.
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Best Local Similarity 100.
Matches 9; Conservative
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11arity 83.3%; Score 8.8; DB ilarity 83.3%; Pred. No. 64; Conservative 0; Mismatches
                                             /mol_type="unassigned DNA"
                                organism="unknown"
      Location/Qualifiers
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**Rothberg, J. Marc., Deem, M. W. and Simpson, J. W.

**Rothberg, J. Marc., Deem, M. W. and Simpson, J. W.

**Method and apparatus for identifying, classifying, or quantifying

**DNA sequences in a sample without sequencing

**Patent: US 5871697-A 18 16-FEB-1999;

**Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (Dases 1 to 12)

Rothberg, J.Marc., Deem, M.W. and Simpson, J.W.

Rothberg, J.Marc., Deem, M.W. and Simpson, J.W.

Method and apparatus for identifying, classifying, or quantifying

DNA sequences in a sample without sequencing

Parent: US 5871697-A 20 16 FEB-1999;

Location/Qualifiers
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Unclassified.
Unclassified.
1 (Dess 1 to 12)
Rothberg,J.Marc., Deem,M.W. and Simpson,J.W.
Rothberg,Gr identifying, Classifying, or quantifying DNA sequencing
sequences in a sample without sequencing
Patent: US 5972693-A 18 26-OCT-1999;
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Pred. No. 64;
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Sequence 18 from patent US 5972693.
AR082060
AR082060.1 GI:10008786
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/organism="unknown"
/mol_type="unassigned DNA"
                             12 bp
Sequence 18 from patent US 5871697.
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Sequence 20 from patent US 5871697,
AR034978.1 GI:5951646
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/wol_type="unassigned DNA"
                                                                      AR034976.1 GI:5951644
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Best Local Similarity 83.3%;
Matches 10; Conservative (
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Best Local Similarity
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AR082060
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RESULT 59
AR034976
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AR034978
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Unclassified.

1 (bases 1 to 12)

Rothberg, J. Marc., Deem, M. W. and Simpson, J. W.

Rothberg, J. Marc., Deem, M. W. and Simpson, J. W.

Method and apparatus for identifying classifying or quantifying DNA sequences in a sample without sequencing sequences in a sample without sequencing Patent: US 6141657-A 18 31-0cT-2000;

Location/Qualifiers
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1 (bases 1 to 12)

1 (bases 1 to 12)

Rothberg, J.Marc., Deem, M.W. and Simpson, J.W.

Apparatus for identifying, classifying, or quantifying DNA

sequences in a sample without sequencing

Patent: US 5972633-A 20 26-OCT-1999;

Location/Qualifiers
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Best Local Similarity 83.3%; Fred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels
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Pred. No. 64;
0; Mismatches
                                                                                                                                    12 bp I
Sequence 20 from patent US 5972693.
AR082062
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Sequence 18 from patent US 6141657.
AR118451
AR118451.1 GI:14099357
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Best Local Similarity 83.3%;
Matches 10; Conservative
5 ACTCGCTGGCAC 16
                                    1 AGTCGCTGGTAC 12
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1 (bases 1 to 12)
Rothberg, J.Marc., Nallur, G.N. and Hu.X.
Methods and devices for measuring differential gene expression
Patent: US 6355423 A 22 12-MAR-2002;
Location/Qualifiers
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1 (bases 1 to 12)

Rothberg,J.Marc., Nallur,G.N. and Hu,X.

Rothberg,J.G.Marc., Nallur,G.N. and Hu,X.

Methods and devices for measuring differential gene expression

Patent: US 6355423-A 24 12-MAR-2002;

Location/Qualifiers
                                                                 Score 8.8; DB 1; Length 12;
Pred. No. 64;
0; Mismatches 2; Indels
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44.0%; Score 8.8; DB
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches
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Seguence 22 from patent US 6355423.
AR199166
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llarity 83.3%; Pred. No. 64;
Conservative 0; Mismatches
1. .12
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Sequence 18 from patent US 6418382.
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1 Similarity 83.3%;
10; Conservative
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AR218175
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AR199168
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AUTHORS
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AR199166
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1 (bases 1 to 12)
1 (bases 1 to 12)
1 Acthberg.'nMarc., Deem,M.W. and Simpson,J.W.
Rothberg.'nMarc., Deem,M.W. and Simpson,J.W.
Rothberg and apparatus for identifying classifying or quantifying DNA
sequences in a sample without sequencing
sequences in a sample without sequencing
Patent: US 6141657-A 20 31-OCT-2000;
Location/Qualifiers
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1 (bases 1 to 12)

Rothberg, J.Marc., Deem, M.W. and Simpson, J.W.

Method and apparatus for indentifying, classifying, or quantifying protein sequences in a sample without sequencing Patent: US 6231812-A 18 15-MAY-2001;

Location/Qualifiers
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                PAT 16-MAY-2001
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Rothberg, J.Marc., Deem, M.W. and Simpson, J.W.
Rothberg, J.Marc., Deem, M.W. and Simpson, J.W.
Rothod and apparatus for indentifying, classifying, or quantifying
protein sequences in a sample without sequencing
Patent: US 6231812-A 20 15-MAY-2001;
Location/Qualifiers
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Pred. No. 64;
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44.0%; Score 8.8; DE
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
               12 bp | Sequence 20 from patent US 6141657.
AR118453
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Sequence 18 from patent US 6231812.
ARISI019.1 GI:15117069
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Sequence 20 from patent US 6231812.
ARIS1021 GI:15117071
                                                                   AR118453.1 GI:14099359
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Matches 10; Conservative
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RESULT 65 AR151019

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ACCESSION VERSION KEYWORDS

RESULT 66 AR151021

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                                                                                                                 Unclassified.

I (bases 1 to 12)

Rothberg,J.M., Deem,M.W. and Simpson,J.W.

Method and apparatus for identifying, classifying, or quantifying

DNA sequences in a sample without sequencing

Patent: US 6418382-A 18 09-JUL-2002;

Location/Qualifiers
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Unclassified.
1 (bases 1 to 12)
1 (bases 3 to 12)
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(Dases 1 to 12)

(Chaberg,J.M., Deem,M.W. and Simpson,J.W.

Method and apparatus for identifying, classifying, or quantifying

DNA sequences in a sample without sequencing

Patent: US 6418382-A 20 09-JUL-2002;
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Pred. No. 64;
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Sequence 18 from patent US 6432361.
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/organism="unknown"
/mol_type="genomic DNA"

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    /mol_type="genomic DNA"

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/organism="unknown"
/mol_type="genomic DNA"
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AR222615.1 GI:23330246
                          GI:23318621
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Matches 10; Conserv
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1 (bases 1 to 12)

Rothberg, J.M., Deem, M.W. and Simpson, J.W.
Rothberg, and apparatus for identifying, classifying, or quantifying protein sequences in a sample without sequencing
Patent: US 6432361-A 20 13-AUG-2002;

Location/Qualifiers
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Rethod and apparatus for identifying, classifying, or quantifying protein sequences in a sample without sequencing protein sequencing protein. US 645245-A 18 17-SEP-2002;
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                                    Length 12;
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44.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 2; Indels
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Sequence 20 from patent US 6453245.
AR231655
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AR222617
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Sequence 18 from patent US 6453245.
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/organism="unknown"
/mol_type="genomic DNA"
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AR231653.1 GI:27272810
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83.3%;
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Best Local Similarity 83.35
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CIZNIS/09, CIZNIS/09, A61K39/00, A61P35/00, A61P37/04, CIZNI/15, PC
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                                                           1. (bases 1 to 12)
Rothberg, J.M., Deem, M.W. and Simpson, J.W.
Rothberg, J.M., Deem, M.W. and Simpson, J.W.
Rothberg, J.M. and apparatus for identifying, classifying, or quantifying protein sequences in a sample without sequencing
Patent: US 6453245-A 20 17-SEP-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 17 15-OCT-2002;
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Location/Qualifiers
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                                                                                                                                                                                            1; Length 12;
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C C12N15/00,C12N5/00,C12N15/00
C Preparation and use of superior vaccines
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Pred. No. 64;
0; Mismatches
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PN JP 2002534056-A/17
PD 15-OCT-2002
PF 18-UUN-1999 JP 2000554749
PR 19-UUN-1998 US 60/090041,19-U1
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JP 2002534056-A/17.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 83.3%;
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BD239966.1 GI:33049736
BD239966.1 GI:33049736
JP 2002534056-A/1384.
Homo sapiens (human)
SM Homo sapiens (human)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Homo sapiens (human)
B Roberts, B.L. and Shankara, S.
E Rob
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PC C12N15/00,C12N5/00,C12N15/00
PC Preparation and use of superior vaccines
FH Key
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Pred. No. 64;
0; Mismatches 1
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Pred. No. 64;
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Best Local Similarity 90.0%;
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Best Local Similarity 90.0%;
Matches 9; Conservative
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C12P21/08,
C12N15/00
Human liver disease-expressing genes
Location/Qualifiers
                                                            Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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19-JAN-2001 JP 2001012328
KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
                                                                                                                                                       BD166770

Human liver disease-expressing genes.

Numan liver disease-expressing genes.

BD166770.

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BD166770.

GD127872582

JP 2002205591-A/315.

SM unidentified

unclassified.

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Matsushimark., Hashimoto,S., Kaneko,S. and Yamashita,T.

Human liver disease-expressing genes

Astent: JP 200220591-A/315

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N JP 200220591-A/315

PF 19-JAN-2001 JP 2001012328

PF 19-JAN-2001 JP 2001012328

PF 19-JAN-2001 JP 2001012328

PC C12N15/09

CC C12N15/09

CC Human liver disease-expressing genes

FH Key

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CC Human liver disease-expressing genes

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Arguntanism='Homo sapiens (h.man)'.

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Arguntanism='Homo sapiens (h.man)'.
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42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 64;
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AX301297.1 GI:17382380
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                                                                                                                                   Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammaila; Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human normal liver cell expression genes
Patent: 'JP 2001211883-A 2 07-Aug-2001;

SCIENCE & TECH AGENCY

SO Homo sapiens (human)

N JP 2001211883-A/2

PD 07-Aug-2001

PF 31-JAN-2000 JP 2000023170

PF 31-JAN-2000 JP 2000023170

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels
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10 bp DNA
Human normal liver cell expression genes.
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Patent: WO 0138577-A 406 31-MAY-2001;
The Johns Hopkins University (US)
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Sequence 11 from Patent WO0185941.

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JP 2001211883-A/2.
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AX301297/c LOCUS DEFINITION

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BD167056.1 GI:27872868
JP 2002209591-A/601.
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N BD166807
N BD166807
Unidentified
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unclassified
unclassified.

1 (baseline).

Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
Human liver disease-expressing genes
Therent: UP 2002209591-A 520 30-JUJ-2002;
JAPAN SCIENCE TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-A/520
PD 30-JUJ-2002
PP 19-JAN-2001 JP 2001012328
PP XOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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organism='Homo sapiens (human)'.
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Human liver disease-expressing genes
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BD166975.1 GI:27872787
Unidentified
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Pred. No. 64;
0; Mismatches
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PC C12N1:
PC C12P2:
PC C12N1:
CC Human
CC Human
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BD166975
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unclassified.

E 1 (and include to 10)

S Mat (baselina, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human liver disease-expressing genes

L Patent: UP 2002209591-A 601 30-UUL-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002209591-A/601

PD 30-UUL-200 D 2001012328

PF 19-JAN-2001 D 2001012328

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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Location/Qualifiers
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Query Match
Best Local Similarity 90.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 1; Indels
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Human liver disease-expressing genes.
BD167056
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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PAT 09-AUG-2002

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Homo sapiens (human)
Memo sapiens
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                 Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 347 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Wethod for determining skin stress or skin ageing in vitro
Patent: Wo dc133773-A 633 11-JUL-2002;
HENKEL KGAA (DE)
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 676 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Sequence 676 from Patent WO02053773.
AX471099.1 GI:22206224
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Sequence 633 from Patent W002053773.
AX471056
AX471056.1 GI:22206181
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Homo sapiens (human)
Homo sapiens
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Homo sapiens
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I (bases 1 to 10)

Matsushimar, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human liver disease-expressing genes

L patent: JP 2002209591-A 729 30-UUL-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

JAPAN SCIENCE AND TECHNOLOGY CORP

JOUL-2002

HOME Sapiens (human)

PN JP 2002209591-A/729

PD 30-UUL-2002

PP 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI YAMASHITA

PC CLENESO, COTKL4/47, COTKL6/18, GOIN33/15, GOIN33/50//CL2P21/02, PC CL2P21/08,

PC CL2NIS/00

CC Human liver disease-expressing genes

PT SOURCE 1. 10

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               C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02, C12P1/08, C12D1/08, C12N15/00
Human liver disease-expressing genes
Key
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C12P21/08,
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Location/Qualifiers
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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Pred. No. 64;
0; Mismatches 1; Indels
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Sequence 347 from Patent WO02053773.
AX470770.1 GI:22205895
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/organism="unidentified"
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/organism="unidentified"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 770 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 1306 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 90.0%; Pred. No. 72;
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Sequence 953 from Patent WO02053774.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 0203774-A 1413 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 0205374-4. 1592 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                  Sequence 3328 from Patent W002053774. AX626287
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AX631454
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AX631632
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053794-A 6531 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 7017 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                             AX629490 11 bp DNA Sequence 6531 from Patent WO02053774.
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AX631333.1 GI:28459379
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Sequence 7017 from Patent WO02053774.
AX629976
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 8375 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Sequence 8496 from Patent WO02053774.
AX631454
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Sequence 8674 from Patent WO02053774.
AX631632
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Matches 9; Conservative
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11 TGGCACGCAC 20 TGGCACGCGC 11 AX631793.1 GI:28459900

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 103 AX631793

Homo sapiens (human) Homo sapiens

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

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DEUGLISS. GI:22636833
S DEUGLISS. GI:22636833
S TP 200152543-A4.6.
Synthetic construct
synthetic construct
artificial sequences.
I (bases 1 to 11)
S Gillies,S.D., Lo,K.M. and Lan,Y.
S Gillies,S.D., Lo,K.M. and Lan,Y.
A Gillies,S.D., Lo,K.M. and Lan,Y.
S Gillies,S.D., Lo,K.M. and Lan,Y.
A Gillies,S.D., Lo,K.M. and Lan,Y.
S Gillies,S.D., Lo,K.M. and Lan,Y.
S Gillies,S.D., Lo,K.M. and Lan,Y.
A LECTOR PRARMACEUTICALS CORP.
OS Artificial Sequence
PN JP 2001525423-A/8
PN 10-DEC-2001;
PF 08-DEC-1998 JP 2000524321
PR 08-DEC-1999 JP 2000524321
PR 08-DEC-1990 JP 20005243
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

E 1 (Basea I to 12)
S Schlingensiepen, K.H., Schlingensiepen, R. and Brysch, W.
A method for stimulating the immune system
Patent: JP 2002517434-A 81 18-JUN-2002;
BICGNOSTIK GESELISCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/81
PD 18-JUN-2002
PF 10-JUN-1999 JP 200553044
PR 10-JUN-1999 BF 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
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                                   PAT 27-AUG-2002
11 bp DNA linear PAT 27-AUG-200:
Hetero dimer fused proteins useful against targeting immunotherapy
and general immunostimulation.
BD091223
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 72;
Matches 9; Conservative 0; Mismatches 1; Indels
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AX631972.1 GI:28467587

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RESULT 104 AX631972 LOCUS

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Query Match Best Local Similarity

TGGCAGGCAC 11

Homo sapiens (human)

Homo sapiens

TITLE JOURNAL

FEATURES

REFERENCE AUTHORS 11 TGGCACGCAC 20

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RESULT 105 BD091223

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PAT 12-DEC-1997

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1 (bases 1 to 10)
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Nose, M. and Duerst, M.
DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
PATENT: WO 9823775-A 3 04-JUN-1998;
DEUTSCHEG KREBSFORSCH (DE); NEES MATTHIAS (DE)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                           Bartnik, E.D. and Margerie, D.D. Regulated genes by stimulation of chondrocytes with 1L-1beta Patent: EP 0705842-A 64 10-APR-1996; HOEGHST AG (DE)
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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Other publication JF 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.

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A52274
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Sequence 3 from Patent WO9823775.
A91804
A91804.1 GI:6740684
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Sequence 4 from Patent W09915680.
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A91804/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Profiling of the immune gene repertoire
Patent: WO 03044225-A 130-MAY-2003;
Bayer Aktiengesellechaft (DE)
Location/Qualifiers
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AX767991. GI:32436671

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Austin, R. C. , Hirsh, J. and Weitz, J. I.
Austin, R. C. , Hirsh, J. and Weitz, J. I.
Methods and compositions for diagnosis of hyperhomocysteinemia
Methods and compositions for CCT-1998;
Datent: US 5817461-A 4 06-OCT-1998;
Location/Qualifiers
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Roberts, J. A. and Paul, W.
CONTROL OF PLANT ABGISSION AND POD DEHISCENCE OR SHATTER
PATENT: WO 9915680-A 4 01-APR-1999,
BIOGEWMA UK LIMITED (GB); ROBERTS JEREMY ALAN (GB)
1 ocation/Qualifiers
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Unknown.
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Smith, M.S. and Chen, L.-C.
Methdy for identifying genes amplified in cancer cells
Patent: US 5776683-A 14 07-JUL-1998;
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Matches 8; Conservative 0; Mismatches 0; Indels
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iive 0; Mismatches
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Sequence 14 from patent US 5776683.
AR016246.1 GI:3972523
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Sequence 4 from patent US 5817461.
AR044027
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1 (bases 1 to 10)
Tam,S.-Y., Tsai,M. and Galli,S.J.
Tam,S.-Y. Tsai,M. and Palli,S.J.
Tam,S.-Y. Section and Calli,S.J.
Fatent: US 5565707-A 3 12-OCT-1999;
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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Sequence 28 from patent US 6077948.
AR099718
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/organism="unknown"
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                                                                                                                                                          Sequence 13 from patent US 5965409.
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AR079528
AR079528.1 GI:10006272
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                                                         7 TCGCTGGC 14
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AR099718/C
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BD239869.1 GI:33049639
JP 2002534056-A/1287.
Homo sapiens (human)
Homo sapiens
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JP 2002534056-A/1924.
Homo sapiens (human)
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 CGCTGGCA 15
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Unknown.
Unclassified.
1 (John 1978)
Russell, M.E. and Utans, U.
Mediators of chronic allograft rejection (AIF-1) and DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 10)
Austin,R.C., Hirsh,J. and Weitz,J.I.
Methods and compositions for diagnosis of hyperhomocysteinemia
Patent: US 6122965-A 4 17-OCT-2000;
                                                                                                                                                                                  Gaps
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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Location/Qualifiers
                                                                            Patent: US 6077948-A 28 20-JUN-2000;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 55 from patent US 6284466.
AR167221 GI:16243735
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Sequence 4 from patent US 6132965.
AR113051
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1 (bases 1 to 10)
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9 TCGCTGGC 2
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AR113051/C
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AR167221/c
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19-UTM-1998 US 60/089997,19-UTM-1998 US 60/080999 RR
19-UTM-1998 US 60/089992,19-UTM-1998 US 60/089993 RR
19-UTM-1998 US 60/08992,19-UTM-1998 US 60/089991 RR
19-UTM-1998 US 60/08992,19-UTM-1998 US 60/089991 RR
19-UTM-1998 US 60/08000,19-UTM-1998 US 60/080048 RR
19-UTM-1998 US 60/080999,19-UTM-1998 US 60/080048 RR
19-UTM-1998 US 60/080984,19-UTM-1998 US 60/080036 RR
19-UTM-1998 US 60/080080,19-UTM-1998 US 60/08037 RR
19-UTM-1998 US 60/080080,19-UTM-1998 US 60/080077 RR
19-UTM-1998 US 60/080080,19-UTM-1998 US 60/080077 RR
19-UTM-1998 US 60/080078,19-UTM-1998 US 60/080077 RR
19-UTM-1998 US 60/080077 RR
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PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/56, PC G01N37/00, C12N15/00, C12N15/0
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(bases 1 to 10)

Roberte, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1287 15-OCT-2002;
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Preparation and use of superior vaccines.
BD239869
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100.0%; Pred. No. 80;
iive 0; Mismatches
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JP 2005534056-A/1287
15-OCT-2002
18-JUN-1999 US 60/09003
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Gaps

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PAT 07-0CT-1996

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Unclassified.
1 (Dases 1 to 10)
Russell, M. B. and Utans, U.
Mediators of chronic allograft rejection and DNA molecules encoding
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Unknown.
Unclassified.
Unclassified.
Liang, P., Fardes, A.B. and Bianchi, C.F.
Liang, P., fardes, A.B. and Bianchi, C.F.
Method & differential display of exposed mRNA by RT/PCR
Patent: US 5599672-A 13 04-FEB-1997;
Location/Qualifiers
        PI HAI CHUA
CC C12N15/00,C12N5/10,C12N15/00,C12N5/00 CC
C2N15/00 Attlficial Sequence Primer API FH Key
Location/Qualifiers 1..10
FT source /organism='Artificial Sequence'.
                                                                                                                                                                ce 1. .10 /organism='Artificial Sequence'. Location/Qualifiers
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100.0%; Pred. No. 80;
ative 0; Mismatches
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Location/Qualifiers
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Matches 8; Conservative 0; Mismatches
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Sequence 28 from patent US 5527884.
122447 12447.1 GI:1602801
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Sequence 13 from patent US 5599672.
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134793/c
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Dasas 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1924 15-OCT-2002;
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Query Match

40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 80;

Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            OS Homo eaptens (human)
PN JP 2002534056-A/1924
PN JP 2002534056-A/1924
PD 15-CT-2002
PF 19-UN-1999 US 60/090039,19-UW-1998 US 60/090035,19-UW-1998 US 60/090035,19-UW-1998 US 60/090035,19-UW-1998 US 60/090035,19-UW-1998 US 60/090000,19-UW-1998 US 60/090000,19-UW-1998 US 60/090000,19-UW-1998 US 60/090000,19-UW-1998 US 60/090042,19-UW-1998 US 60/090042,19-UW-1998 US 60/090044,19-UW-1998 US 60/090080,19-UW-1998 US 60/090080,19-UW-1998 US 60/090080,19-UW-1998 US 60/090076,19-UW-1998 US
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Preparation and use of superior vaccines
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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PAT 13-MAY-1997

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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RESULT 121 BD248338/c LOCUS

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synthetic construct
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artificial sequences.
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Best Local Similarity
Matches 8; Conserv
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AX016299/c
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Romick, T. L. and Fraser, M.S.
PCR technique for detecting microbial contaminants in foodstuffs Patent: US 6468743.A 13.2 22-OCT-2002;
Location/Qualifiers
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40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels
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Pardee, A.B. and Liang, P.
Methods of comparing levels or amounts of mRNAs
Patent: US 5665547-A 13 09-SEP-1997;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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Sequence 132 from patent US 6468743.
AR238724 1GI:27283794
                                                                                  Sequence 13 from patent US 5665547.
164511
164511.1 GI:2481405
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/organism="unknown"
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Sequence 3 from patent US 6500942.
AR270938
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1 (bases 1 to 10)
Tam,S.-Y., Tsai,M. and Galli,S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
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Unclassified.
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Unclassified.
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                   TCGCTGGC 2
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AR238724/c
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AR270938/C
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I64511/c
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Rin2, a novel inhibitor of Ras-mediated signaling
Patent: US 6500942-A 3 31-DEC-2002;
Location/Qualifiers
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Patent: WO 0138577-A 83 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Arbitrary primer A"
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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llarity 100.0%; Pred. No. 80;
Conservative 0; Mismatches
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/mol_type="unassigned DNA"
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Sequence 83 from Patent WO0138577.
AX152168.1 GI:14533819
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Sequence 2 from Patent W09949046.
AX016299

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    /organism="unknown"
    /mol_type="genomic DNA"

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Unknown.
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BD107610/c
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AR023571
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PN 472201509917-A/221
PD 10-7UL-2015
PF 22-JAN-1999 UP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT V VGELSTEIN, KENNETH W KINZLER PC CLANIS/10, C12NIS/31, C07KH4/395, C12Q1/68, C12Q1/62 CC Characterization of the yeast transcriptome
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Characterization of the yeast transcriptome.
BD065285
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Similarity 100.0%; Pred. No. 80;
8; Conservative 0; Mismatches
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                    Strandedness: Single;
Topology: Linear;
/desc = 'Primer'
                                                                                                  BD023238.1 GI:22564461
JP 2001504703-A/3.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BD065285.1 GI:22610888
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                       ATGGACTC 10
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Matches 8; Conserv
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Synthetic construct

ISM synthetic construct

artificial sequences.

CE 1 (bases 1 to 10)

RS Yamamoto, T., Sawamura, Y., Imai, T., Matsuda, N., Saito, T., Shoda, M.,

Rotobuki, K., Hayashi, K., Ba, Y., Kozono, M. and Kimura, T.

Rotobuki, K., Hayashi, K., Ba, Y., Kozono, M. and Kimura, T.

Rotobuki, K., Hayashi, K., Ba, Y., Kozono, M. and Kimura, T.

Rotobuki, K., Hayashi, K., Ba, Y., Kozono, M. and Kimura, T.

Rotobuki, R., Hayashi, K., Ba, Y., Kozono, M. and Kimura, T.

Rotobuki, R., Hayashi, K., Ba, Y., Kozono, M. and Kimura, T.

Rotobuki, R., Hayashi, R., Ba, Y., Kozono, M. and Kimura, T.

Rotopuki, R., Hayashi, M. Artificial Sequence Primer

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PI TOSHIYUKI BAN,

PI TOSHIYUKI BA
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                               ce 1..10 /organism='Saccharomyces carevisiae (yeast)'. Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches
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Sequence 39 from patent US 5795716.
AR023571. GI:3976865
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BD107610.1 GI:23202428
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M Unknown.
Unclassified.

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Sequence 365 from Patent WO02053773.
AX470788
AX470788.1 GI:22205913
                                                                                    Sequence 312 from patent US 6538173.
AR301731.
AR301731.1 GI:31689533
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Sequence 39 from patent US 6607887.
AR381088
AR381088.1 GI:40088812
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/organism="unknown"
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Unclassified.
1 (bases 1 to 11)
Chee,M.S.
 10 CIGGCACG 17
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Matches 8; Conserv
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Patent: US 6242180-A 39 05-JUN-2001;
Location/Qualifiers
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1 (bass 1 to 11)
Chee.M.S.
Computer-aided visualization and analysis system for sequence
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Patent: US 5974164-A 39 26-OCT-1999;
Location/Qualifiers
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40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches
                                             Comparation
Patent: US 5795716-A 39 18-AUG-1998;
Location/Qualifiers
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Sequence 39 from patent US 5974164.
AR082679
AR082679.1 GI:10009399
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/organism="unknown"
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Sequence 39 from patent US 6242180.
ARIS6206.
ARIS6206.1 GI:15124910
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/organism="unknown"
/wol_type="unassigned DNA"
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Unclassified.
1 (bases 1 to 11)
Chee,M.S.
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AR082679
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AR156206
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PAT 12-JUN-2003
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: US 6607887-A 39 19-AUG-2003;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels
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AX471851/c
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AX623074
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AX624694/c
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           Hofmann, K., Conzadt, M. and Petersohn, D.

Method for determining skin stress or skin ageing in vitro
Patent: WO 0203773-A 365 11-JUL-2002;

HENKEL KGAA (DE)

Location/Qualifiers
1. 11

/organism="Homo sapiens"
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1384 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 89;
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Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches
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Sequence 851 from Patent W002053773.
AX471274
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bethod for determining skin stress or skin ageing in vitro
Patente: WO 0205773-A 1428 11-UUL-2002;
HENKEL KGAA (DE)
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Query Match
40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches
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Homo sapiens
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KEYWORDS SOURCE ORGANISM

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Gaps ; 0 PAT 21-FEB-2003

linear

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 100.0%; Fred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indols
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Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indols
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    Method for determining homeostasis of the skin
Patent: WO 0203374-4-8 2099 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 2741 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 2741 from Patent WO02053774.
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AX625700/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 1955 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
Sequence 1735 from Patent WO02053774.
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Petersohn, D., Conradt, M. and Hofmann, K.
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Sequence 2099 from Patent W002053774.
AX625058
AX625058.1 GI:28452999
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                                                                 AX624694.1 GI:28452635
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

RESULT 143 AX624914 LOCUS

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RESULT 144
AX625058/c
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KEYWORDS

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REFERENCE AUTHORS

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Gaps

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PAT 21-FEB-2003

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AX628487/c LOCUS

RESULT 147

Matches

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                          Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches 8; Conservative 0; Mismatches 0; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 7784 11-JUL-2002;
Henkel Kommanditgeeellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                               Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A.
Henkel Kommanditgeeellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 7536 11-JUL-2002;
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AX629743.1 GI:28457781
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                                                           Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                      AX628487 11 bp DNA Sequence 5528 from Patent W002053774. AX628487
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches

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    /organism="Homo sapiens"
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    /db_xref="taxon:9606"

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/db_xref="taxon:9606"
  0; Mismatches
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8; Conservative
                                     9 GCTGGCAC 16
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AX629639/c
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AX628761/c
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AX632796 11 bp DNA Sequence 9838 from Patent WO02053774. AX632796 GI:28468411
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100.0%; Pred. No. 89;
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Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches

    .11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.(
Matches 8; Conservative
11 TGGCACGC 18
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                            1 TGGCACGC
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AX632796/c
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AX632794/c
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AX632479/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                            Length 11;
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 9377 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 9157 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches
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Sequence 9377 from Patent WO02053774.
AX632335
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40.0%; Score 8; DB 1,
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches

    .11
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Homo sapiens
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Best Local Similarity 100.
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AX632115/c
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AX632335
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                                                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                              Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 9521 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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AX632479 11 bp DNA Sequence 9521 from Patent W002053774. AX632479
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RESULT 157

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Unknown.
Unclassified.
1 (bases 1 to 12)
Hiatt,A.C. and Rose,F.D.
De novo polynucleotide synthesis using rolling cemplates
Patent: US 6.135588-A 5 24-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.0%; Score 7.8; DB 1;
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Sequence 4 from patent US 5474897.
I16095.
I16095.1 GI:1251003
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Sequence 8 from patent US 6288142.
AR168866
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              AR135803.1 GI:14476475
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AR168866/c
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PN 7P 2002503460-A/312

PD 05-FEB-1002 3D 2000531545

PF 12-FEB-1999 JP 2000531545

PR 13-FEB-1999 US 60/097937 PR 60/102051

PR 13-FEB-1999 US 60/102051
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DFD124481.1 GI:23219426
UP 2002503460-A/312.

Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

Katz, E.H.
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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40.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                           Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 9838 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)
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Patent: JP 2002503460-A 312 05-FEB-2002;
THE WISTAR INSTITUTE
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Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 5 from patent US 6136568.

    ..11
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /db_xref="taxon:10090"

            Homo sapiens (human)
Homo sapiens
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Unclassified.
Unclassified.
Unclassified.
Weiss,and Fraser,J.
Weiss,A. and Fraser,J.
Screening assay for the identification ov novel immunosuppressives
Screening stated T cells
Patent: US 5474897-A 4 12-DEC-1995;
Patent: US 5474897-A 4 12-DEC-1995;
Location/Qualifiers
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Length 1.2;
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Bugnon,P. and Herren,F.
Process for warp-free pigmenting of polyolefins
Patent: US 6288142-A 8 11-SEP-2001;
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PAT 21-FEB-2003

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PAT 21-FEB-2003

KEYWORDS SOURCE ORGANISM

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REFERENCE AUTHORS TITLE JOURNAL

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AX319383/c LOCUS

RESULT 161

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Homo sapiens
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primetes; Catarrhini; Hominidae; Homo.
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Staryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                      Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 1343 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
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Sequence 1343 from Patent WO02053773.
AX471766
AX471766.1 GI:22206891
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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Best Local Similarity 81.8
Matches 9; Conservative
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AX623493
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                      Hypocrea jecorina
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
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Method for determining skin stress or skin ageing in vitro
Patente: WO 0205773-A 324 11-JUL-2002;
HENKEL KGAA (DE)
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Conservative 0; Mismatches 2; Indels
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Sequence 324 from Patent WO02053773.
AX470747
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/organism="Homo sapiens"
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          Pred. No. 99;
0; Mismatches
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Sequence 55 from Patent WO0172783.
AX319383
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            81.8%;
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            Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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RESULT 163 AX471766 LOCUS

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 162 AX470747 LOCUS

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PAT 21-FEB-2003
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 99;
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Method for determining homeostasis of the skin
Patent: WO 2053774-A 3075 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 3325 11-JUL-2002, Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
                                                                                                                                      Sequence 3075 from Patent WO02053774.
AX626034.1 GI:28454072
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Sequence 4701 from Patent WO02053774.
AX627660
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/organism="Homo sapiens"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Homo sapiens
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Find 9; Conservative
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AX627660/c
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AX626034
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AX626284
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 2023774-4 1447 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
Patent: WO 02053774-A 732 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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REFERENCE AUTHORS TITLE JOURNAL

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Homiwidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053794-A 7955 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 7955 from Patent WO02053774.
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AX631112
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 6201 11-UUL-2002;
Patents Kommanditgesellschaft auf Aktien (DE)
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Method for determining homeostasis of the skin
Patent: WO 02053774-4458 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                              Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 4701 11-TUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Sequence 4858 from Patent WO02053774.
AX627817
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Sequence 6201 from Patent W002053774.
AX629160
AX629160.1 GI:28457198
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REFERENCE AUTHORS

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NETHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM BY REVENEE TRANSCRIPTION-POLYMERASE CHAIN REACTION
RNAL PATENT: NO 9813521-A 78 02-APR-1998;
PESCE RICCARDO (IT)
Location/Qualifiers
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CHIMARIC CLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION
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PACENT: WO 9710332-A 49 20-MAR-1997;
BRAX GENOMICS IND (GB)
Location/Qualifiers
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Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Patent: WO 9001548-A 18 22-FEB-1990;
Location/Qualifiers
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Sequence 78 from Patent WO9813521.
A71519.1 GI:4775131
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12 bp
Aequence 49 from Patent W09710332
A61480
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 99;
0; Mismatches 2; Indels
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39.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 8938 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
                                                                                              Sequence 8869 from Patent WO02053774.
Ax631827.1 GI:28459934
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Sequence 8938 from Patent W002053774.
AX631896 1 GI:28460034
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Part linker.
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A06190.1 GI:411222
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AX631827/c
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AX631896/c
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A06190/c
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PAT 07-MAY-1999

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Gaps

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REFERENCE AUTHORS TITLE JOURNAL

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Matches

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B29701 12 bp DNA linear PAT 18-JUN-2001 Method for amplifying DNA fragment, method for estimating state of microorganism existing and method for estimating state of waste.
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                                                                                             Inoue.T.

Inoue.T.

Method of amplifying DNA fragment, apparatus for amplifying DNA fragment, method of assaying microorganisms, method of analyzing microorganisms and method of assaying contaminant

Datent: US 6287769-A 181 11-SEP-2001;

Location/Qualifiers
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
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AR167817.1 GI:17903622
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E29701.1 GI:13021204
JP 1999276176-A/181.
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                                       Unknown.
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Unclassified.
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1 (bases 1 to 12)
Nandabalan, K. and Rothberg, J. Marc.
Identification and comparison of protein-protein interactions that occur in populations
Patent: US 6083693-A 79 04-UUL-2000;
Location/Qualifiers
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Nandabalan, K. and Rothberg, J.Marc.
Mandabalan, K. and comparison of protein-protein interactions that occur in populations
Patent: US 6083693-A 78 04-JUL-2000;
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Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Pred. No. 1.1e+02;
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Sequence 181 from patent US 6287769.
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Sequence 79 from patent US 6083693.
AR100991
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Sequence 78 from patent US 6083693.
AR100990.
AR100990.1 GI:12811788
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RESULT 181 AR100991

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RESULT 182 AR167817 LOCUS DEFINITION

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AR371423
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AR199084
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Datent: JP 1999141989-A 181 14-DEC-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY BLOW FISHERIES
OS Artificial Sequence
PP 1999341989-A/181
PD 1999341989-A/181
PP 16-MAR-1999 JP 1999069694
PR ROICHI INOUR
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC FH Key Location/Qualifiers
FT Source /organism='Artificial Sequence'.
                                                                                                                                                  Method and device for amplifying DNA fragment
Patent: JP 200270867-A 181 03-OCT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHBRIES
OS Unidentified
FN JP 200270867-A/181
FD 03-OCT-2000
FP 19-MAR-1999 JP 1999076844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 bp DNA linear PAT 18-JUN-2001 Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for analyzing a group of microorganisms, and method for assaying contaminating substance.
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Method and device for amplifying DNA fragment.
E38807
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C12N15/09,C12M1/00,C12Q1/68,C12N15/00
Strandedness: Single;
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    .12
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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E64233.1 GI:13019637
UP 199341899-A181.
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artificial sequences.
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                                          E38807.1 GI:18621469
JP 2000270867-A/181.
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1 (bases 1 to 12)
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E64233
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Chimeric oligonucleotides and uses thereof in the identification of antisense binding stees
Patent: US 6355418-A 32 12-MAR-2002;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 12)
Nandabalan,K. and Rothberg,J.M.
Nandabalan,K. and comparison of protein-protein interactions that occur in populations and indentification of inhibitors of these interactors
Interactors
Patent: US 6395478-A 78 28-MAY-2002;
Location/Qualifiers
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Best Local Similarity 81.8%; Pred. No. 1.18+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                       Length 12;
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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                                                                                                     Query Match 39.0%; Score 7.8; DB 1; Best Local Similarity 81.8%; Pred. No. 1.1e+02; Matches 9; Conservative 0; Mismatches 2

    12
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/mol type="genomic DNA"
/db_xref="taxon:32630"

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                                                                                                                                                                                                                                                                                                  Sequence 32 from patent US 6355418.
AR199084
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Sequence 78 from patent US 6395478.
AR371423. GI:34608357
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/organism="unknown"
/mol_type="unassigned DNA"
Location/Qualifiers
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Best Local Similarity 81.8%;
Matches 9; Conservative C
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  Hustert, E., Wojnowski, L. and Biselt, R.
Polymorphisms in the human cyp3a4, cyp3a7 and hpxr genes and their use in diagnostic and therapeutic applications
Patent: EP 1088900-A 65 04-APR-2001;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Patent: WO 02063030-A 57 15-AUG-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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Pred. No. 1.1e+02;
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/wol_type="unassigned DNA"
                                                                                                                                                                     1. .12 | Organism="synthetic construct" | /organism="synthetic construct" | /mol_type="unassigned DNA" | /db xref="taxon:32630" | /nole="DNA" 
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Primer tail"
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Sequence 663 from Patent WO0202606.
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Sequence 57 from Patent W002063030.
AX698726 AX698726.1 GI:29499514
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AX350140.1 GI:18615818
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                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 12)
Nandabalan, K. and Rothberg, J.M.
Mandabalan, K. and comparison of protein-protein interactions that occur in populations and indentification of inhibitors of these interactors
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Polymorphisms in the human hpxr gene and their use in diagnostic and therapeutic applications
Patent: WO 0120026-A 29 22-MAR-2001;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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/db_xref="reaxon:32630"
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Location/Qualifiers
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Sequence 79 from patent US 6395478,
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Sequence 65 from Patent EP1088900.
AX136991 GI:14273338
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Sequence 29 from Patent W00120026.
AX098966
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AR371424.1 GI:34608358
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AX136991/c
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AX098966/c
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Synthetic construct
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artificial sequences.

E | (bases 1 to 12)
Saito, I., Fujimoto, K., Matsuda, S. and Yoshino, H.

5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same
patent: JP 2001348398-A 4 18-DEC-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Artificial Sequence
PN JP 2001343398-A/4
PD 18-DEC-2001
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                     Score 7.8; DB 1; Length 12;
Pred. No. 1.18+02;
0; Mismatches 2; Indels
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/organism="synthetic construct"
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db_xref="taxon:32630"
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BD105403.1 GI:22650977
JP 2001348398-A/3.
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BD105404.1 GI:22650978
                       39.0%;
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Best Local Similarity 81.8
Matches 9; Conservative
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N BD10540', D122650991
NS BD10540', D1348398-A/7.
Springer construct
artificial sequences.
NE Saito, L' Fujimcto, K., Matsuda, S. and Yoshino, B.
Saito, L' Fujimcto, K., Matsuda, S. and Yoshino, B.
S-Pyrimidine-containing nucleic acid, and reversible ligation method using the same method using the same method using the same method using the same parent: 197 2001348398-A/7
N Artificial Sequence
N Artificial Sequence
P 05-JAN-2001 JP 2001000750
P 18-DEC-2001
P 05-JAN-2001 JP 2001000750
P 18-DEC-2001
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0; Mismatches 2; Indels
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Sequence 2216 from Patent WO0242459.
AX668767 1 GI:29291742

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Matches 9; Conservative
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Unknown.
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Position dependent recognition of gnn nucleotide triplets by zinc fingers
fingers
Patent: WO 0242459-A 2216 30-MAY-2002;
Sangamo Biosciences Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                               Liu.Q.
Destrion dependent recognition of gnn nucleotide triplets by zinc fingers
Fingers WO 0242459-A 2286 30-MAY-2002;
Patent: WO 0242459-A (US)
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Sequence 2286 from Patent WO0242459.
AX668837
AX668837.1 GI:29291812
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Sequence 2287 from Patent WO0242459.
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AX668838
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Unclassified.
1 (bases 1 to 10)
Ecker, D.J., Bruice, T.W. and Vickers, T.A.
Reagents and methods for modulating gene expression through RNA mimicry
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37.0%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred, No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                           Query Match 37.0%; Score 7.4; DB 1; Length 9; Best Local Similarity 88.9%; Pred. No. 7.7e+02; Matches 8; Conservative 0; Mismatches 1; Indols
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/db xref="taxon:32630"
/noTe="example target DNA"
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1 (bases 1 to 10)
Eaton,B.E. and Gold,L.
Parallel selex
Patent: Location/Qualifiers
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/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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Location/Qualifiers
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Sequence 1 from patent US 5789160.
AR020450
AR020450.1 GI:3975065
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Sequence 4 from patent US 5736294.
AR000035
AR000035.1 GI:3962566
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Unclassified.
1 (bases 1 to 10)
2avda,J., Pastorekova,S. and Pastorek,J.
Zavdada,J., Pastorekova,S. and Pastorek,J.
Pavent: US 5972353-A 21 26-OCT-1999;
Patent: US 5972353-A 21 26-OCT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 10)

2 Vavda, J., Pastorekova, S. and Pastorek, J.

Method of inhibiting tumor growth using antibodies to MN protein
Patent: US 5955075-A 21 21-SEP-1999;

Location/Qualifiers
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   DNA
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1 (bases 1 to 10)
Eston, B. and Gold, L.
Parallel selex
Patent: US 5858660-A 1 12-JAN-1999;
Location/Qualifiers
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Sequence 21 from patent US 5955075.
AR074450 AR074450.1 GI:10001205
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 AR028150 10 bp
Sequence 1 from patent US 5858660.
AR028150 GI:5940123
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Best Local Similarity 88...
Best Local 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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Zavada, J., Pastorekva, S. and Pastorek, J.
Immunological methods of detecting MN proteins and MN polypeptides
Patent: US 5989838-A 2. 123-NOV-1999,
Location/Qualifiers
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A Score 7.4; DB 1; Length 10; Similarity 88.9%; Pred. No. 1.1e+02; 8; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.16+02;
0; Mismatches 1; Indels
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Unclassified.
1 (bases 1 to 10)
Zavada,J., Pastorekova,S. and Pastorek,J.
MN-specific antibodies and hybridomas
Patent: US 5987711-A 21 09-NOV-1999;
Location/Qualifiers
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AR085327
AR085327.1 GI:10012096
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/organism="unknown"
/wol_type="unassigned DNA"
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RESULT 209
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(Dass 1 to 10)

Roberts, B.L. and Shankara, S.
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 202534056-A 133 15-0CT-2002;
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60/090079 PR
60/089993 PR
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M Unknown.
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E 1 (bases 1 to 10)

(S Zavada, J., Pastorekova, S. and Pastorek, J.
Detection and quantitation of MN specific antibodies
(AL Patent: US 6093548-A 21 25-JUL-2000;
Location/Qualifiers
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88.9%; Pred. No. 1.18+02;
iive 0; Mismatches 1; Indels
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BD238715.
BD238715.1 GI:33048485
Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 10)

2 savada, ..., Pastorekova, S. and Pastorek, J.

MN gene and protein

Patent: US 6204370-A 21 20-MAR-2001;

Location/Qualifiers
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BD239057.1 GI:33048827
BD239057.1 GI:33048827
BD239057.1 GI:33048827
Homo sapiens (human)
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Experiments of to 10;
Broberts, B.L. and Shankara.S.
Preparation and use of Superior vaccines

Patent: JP 2002534056-A 475 15-OCT-2002;
BM JP 2000534056-A 475 15-OCT-2002;
BM JP 200054149
19-JUN-1998 US 60/089978,19-JUN-1998 US 60/089991 PR 19-JUN-1998 US 60/080000,19-JUN-1998 US 60/080048 PR 60/080000,19-JUN-1998 US 60/080042 PR 60/080042,19-JUN-1998 US 60/080042,19-JUN-1998 US 60/080042,19-JUN-1998 US 60/08036 PR 19-JUN-1998 US 60/080044,19-JUN-1998 US 60/089844 PR 60/08080,19-JUN-1998 US 60/089844 PR 60/08080,19-JUN-1998 US 60/080047 PR 60/080078,19-JUN-1998 US 60/080047 PR 60/080078,19-JUN-1998 US 60/080047 PR 60/117715 PR FIRECTION CONTRACTOR CONTR
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.larity 88.9%; Pred. No. 1.1e+02;
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Preparation and use of superior vaccines.
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           19-70N-1998 US
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RESULT 212
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C12N15/00,C12N5/00,C12N15/00
Preparation and use of superior vaccines
Key Location/Qualifiers
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1 (bases 1 to 10)
Preparation and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 479 15-0CT-2002;
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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Preparation and use of superior vaccines
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18-JUN-1999 JP 2000554749
19-JUN-1998 US 60/09003
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JP 2002534056-A/479
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JP 2002534056-A/479.
Homo sapiens (human)
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LOCUS
DEFINITION
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VERYORDS
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AUTHORS
TITLE
JOURNAL
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TITION Preparation and use of superior vaccines.

NO BD239128

NO BD239128

NO BD239128

NO BD239128.1 GI:33048898

NO BD239128.1 GI:33048898

NO BD239128.1 GI:33048898

NO SAP 2002534056-A/546.

Homo sapiens (human)

NISM Homo sapiens (human)

NISM Homo sapiens (human)

NISM Homo sapiens (human)

TOE I (bases 1 to 10)

RS Roberts B.L. and Shankara, S.

Preparation and use of superior vaccines

NI Patent: JP 2002534056-A 546 IS-OCT-2002;
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Score 7.4; DB 1; Length 10;
Pred, No. 1.1e+02;
0; Mismatches 1; Indels
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Preparation and use of superior vaccines
Key
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002534056-A/546
15-OCT-2002
    37.0%;
88.9%;
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         Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Location/Qualifiers
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synthetic construct
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PD 15-0CT-2000

PT 18-CUN-1999

PR 19-CUN-1999

19-CUN-1999 US

19-CUN-1998 US
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BD270828
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BD270828
LOCUS
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AUTHORS TITLE
JOURNAL
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                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 10)

Roberts, B.L. and Shankara, S.
Roberts, B.L. and Shankara, S.
Perparation and use of superior vaccines
Patent: JP 2002534056-A 567 15-OCT-2002;

GENZYMB CORP
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I (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1224 15-OCT-2002,
GENZYME CORP
OS Homo sapiens (human)
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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60/089993
60/089993
60/090943
60/08984
60/08984
60/089844
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60/089853
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88.9%; Pred. No. 1.1e+02;
tive 0; Mismatches 1; Indels
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    .10
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/db_xref="taxon:9606"

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JP 202534056-A/567
15-0CT-2090
18-JUN-1999 US 60/090039
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JP 2002534056-A/1224.
Homo sapiens (human)
Homo sapiens
                                GI:33048919
                           BD239149,1 GI:330489
JP 2002534056-A/567.
Homo sapiens (human)
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Best Local Similarity 88.9
Matches 8; Conservative
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PC CI2NI,21,C12NS/10,G01N33/15,G01N33/50,G01N33/53,G01N33/56, PC G01N37/00, C2 C12N15/00,C12N15/00,C12N15/00 C2 Preparation and use of superior vaccines in Location/Qualifiers
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20-AUG-2002
13-SEP-1999 JP 2000574297
21-SEP-1998 US 09/157601
BRUCE BATON THEODORE M TARASOW
COTH21/00, COTB61/00, CI2N15/09, G01N33/15, G01N33/50, G01N33/50//
A61K45/00,
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60/090048 PR
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60/089844 PR
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              05 000041, 19-UNN-1998 US 60/090039, 19-UNN-1998 US 60/090035, 19-UNN-1998 US 60/090032, 19-UNN-1998 US 60/090042, 19-UNN-1998 US 60/090044, 19-UNN-1998 US 60/090044, 19-UNN-1998 US 60/090044, 19-UNN-1998 US 60/090078, 19-UNN-1998 US
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1 (bases 1 to 10)
Eaton, B. and Tarasow, T.M.
Parallel selex
Patent: JP 2002526511-A 1 20-AUG-2002;
INVENUX INC
OS Artificial Sequence
OS Unknown
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/organism="Homo gapiens"
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/db_xref="taxon:9606"
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JP 2000554749
US 60/09000
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Length 10;

PAT 20-JUN-2002

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1 (Dases 1 to 10)
Ecker, D.J., Bruice, T.W. and Vickers, T.
Engants and methods for modulating gene expression through RNA mimicry
Patent: US 636863-A 4 09-APR-2002,
Location/Qualifiers
1 .10
/organism="unknown"
/mol_type="unassigned DNA"
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Unclassified.
Unclassified.
1 (bases 1 to 10)
Hohmann, H.-P., Humbelin, M., van Loon, A. and Schurter, W. Riboflavin production
Patent: US 6322995-A 240 27-NOV-2001;
Patent: Location/Qualifiers
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Sequence 240 from patent US 6322995.
AR261814 GI:28072954
                                                                      Unclassified.
1 (bases 1 to 10)
Baton,B.E. and Gold,L.
Barallel selex
Parent: US 5723592-A 1 03-WAR-1998;
Location/Qualifiers
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Sequence 4 from patent US 6368863.
AR205452
AR205452.1 GI:21503037
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190091.1 GI:3410031
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AR261814/c
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Unclassified.
2 1 (Dasses 1 to 10)
3 Antragenesis methods and compositions
Mutagenesis methods and compositions
AL Patent: US 5702331-A 1 30-DEC-1997;
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
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Woknown.
Unknown.

B 1 (bases 1 to 10)

S Eaton, B.E. and Gold, L.

Parallel selex

Patent: US 5723289-A 1 03-WAR-1998;

Location/Qualifiers

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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 1 from patent US 5702931.
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Sequence 1 from patent US 5723592.
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Sequence 1 from patent US 5723289.
189787
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186912/c
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Homo sapiens (human)
Pumo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 88.9%; Pred. No. 1.18+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Patent: WO 0138577-A 693 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                          relculescu, V.E., Vogelstein, B. and Kinzler, K.W. Human transcriptomes
Patent: WO 013877-4
The John Hopkins University (US)
Location/Qualifiers
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Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
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Patent: WO 0138577-656 31-MAX-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 656 from Patent WO0138577.
AX152741
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1 (bases 1 to 10)
1 (bases 1 to 10)
Dobrindt, D. and Fischer, U.
Dobrindt, D. and Fischer, U.
Patchial Patent: US 6588746-A 567 08-JUL-2003;
Location/Qualifiers
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Dobrindt,D. and Fischer,U.
Device for generating an offset of transported flexible sheet
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 Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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Location/Qualifiers
1. .10
/organism="unknown"
                                                                                                                                                               AR351673 10 bp 10 bp Sequence 567 from patent US 6588746.
AR31673
AR351673.1 GI:33753469
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Sequence 568 from patent US 6588746.
AR351674
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                  5 ACTCGCTGG 13
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                                                                             10 ACGCGCTGG 2
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Best Local Similarity
Matches 8; Conserv
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AR351674/c
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AR351673/c
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PAT 22-JUN-2001

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Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                  Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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Patent: WO 0138577-A 1368 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                                                                                                                    Velculescu, V. E., Vogelstein, B. and Kinzler, K. W.
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Patent: WO 0138577-4 1227 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                10 bp DN
Sequence 1227 from Patent WO0138577.
AXIS3312

    .10
    /organism="Homo sapiens"
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    .10
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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WO0175177.
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AX302591
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Homo sapiens
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Best Local Similarity 88.5.
Best Local Similarity
Conservative
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Best Local Similarity 88.9°
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AX153312
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AX302591/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0.138577-A 1122 31-WAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
                                                                  Query Match
37.0%; Score 7.4; DB 1;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                             10 bp DNA
Sequence 1122 from Patent W00138577.
AX152207.
AX153207.1 GI:14534858
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Patent: WO 0138577-4
The Johns Hopkins University (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/ub_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conserv
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Best Local Similarity
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AX667119/c
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Position dependent recognition of gnn nucleotide triplets by zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Balakireva,L.
Polypeptides inhibiting hepatitis c virus internal ribosome entry bolypeptides inhibiting hepatitis c virus internal ribosome entry site (ires), and method for screening said polypeptides patent: WO 0233376-A 4 25-APR-2002;
PARTEUROP DEVELOPPEMENT (FR)
Location/Qualifiers
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                        Morin, P.J., Sherman-Baust, C.A., Pizer, E.S. and Hough, C.D.
Tumor markers in ovarian cancer
Patent: WO 017517-A 109 11-CCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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/organism="Hepatitis C virus"
/mol type="unassigned DNA"
/db xref="taxon:11103"
/noTe="Sequence de la boucle IIIc"
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Patent: WO 0242459-A 567 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Sequence 567 from Patent W00242459.
AX667118
                                                                                                                      10 bp
Sequence 4 from Patent WO0233376.
AX469413
AX469413.1 GI:21901709
                                                                                                     Location/Qualifiers
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synthetic construct
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Best Local Similarity 88.9
Matches 8; Conservative
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AX667118/c
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AX469413/c
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                                                        TITLE
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                                            AUTHORS
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

In Chases I to 10)

In Chases I to 10)

In Magai, S., Matsushima, K. and Hashimoto, S.
Human activated Th1 and Th2 cell expression genes

In Patent: JP 200186482-A, 139 02-JUL-2002;

PR Human PR CIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002186482-A/139

PD 02-JUL-2002

PP 19-DEC-2000 JP 2000385816

PI SHIGBNORI NAGAI, KOJI MATSUSHIMA, SHINICHI HASHIMOTO PC

C12N15/09, COTX14/47, COTX16/18, C12P21/08, C12N15/00 CC Human activated Th1 and Th2 cell expression genes FH Key

Location/Qualifiers
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Pred. No. 1.1e+02;
0; Mismatches 1
                                                                                                             37.0%; Score 7.4; DB 1;
88.9%; Pred. No. 1.1e+02;
trive 0; Mismatches 1
/organism="synthetic construct"
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Patent: WO 0242459-A 568 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Seguence 568 from Patent WO0242459.
AX667119
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llarity 88.9%;
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synthetic construct
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Homo sapiens (human)
Homo sapiens
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PD 30-20|
PP 19-JAN
PP 19-JAN
PP C12N1
PC C12N1
PC C12N2
PC C12N2
PC C12N2
PC C12N2
PC Human
FH Key
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Bularyota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E (Dases 1 to 10)

S Matsushima, K. and Hashimoto, S.

Human activated Th1 and Th2 cell expression genes

L Patent: JP 2002186482-A 217 02-UIL-2002;

DN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN D 2002186482-A/217

PD 02-UIL-2002

PF 19-DEC-2000 JP 2000385816

PI SHIGENORI NAGAI, TAOJI MATSUSHIMA, SHINICHI HASHIMOTO PC

CLINIS/09, COTXIA/47, COTXIG/18, CL2P21/08, CL2NIS/09 CC

CLINIS/09, COTXIA/47, COTXIG/18, CL2P21/08, CL2NIS/09 COTXIA/17, COTXIG/18, CL2P21/08, CL2NIS/09 COTXIA/17, COTXIG/18, CL2P21/08, CL2NIS/09 COTXIA/17, COTXIG/08, CL2NIS/09 COTXIA/17, COTXIG/08, CL2NIS/09 COTXIA/17, COTXIG/08, CL2NIS/09, COTXIA/17, COTXIG/08, CL2NIS/09, CL2NIS/09, COTXIA/17, COTXIG/08, CL2NIS/09, COTXIA/17, COTXIG/08, CL2NIS/09, COTXIA/17, COTXIG/08, CL2NIS/09, COTXIA/17, COTXIG/08, CL2NIS/08, 
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Location/Qualifiers
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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                                                                                                    h Similarity 88.9%; Score 7.4; DB 1; Similarity 88.9%; Pred. No. 1.1e+02; 8; Conservative 0; Mismatches 1
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Human liver disease-expressing genes.
BD166561
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JP 2002186482-A/217.
Homo sapiens (human)
Homo sapiens
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JP 2002209591-A/106.
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Matches 8; Conserv
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C12N1S/00
Inver disease-expressing genes
Key
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NN Human liver disease-expressing genes.
BD166788.1 GI:27872600

TP 200220591-A/333.

Unidentified

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19-JAN-2001 JP 2001012328
KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
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Location/Qualifiers
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Key Location/Qualifiers
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Human liver disease-expressing genes.
BD166869

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Best Local Similarity 88.5.
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Best Local Similarity
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Tue Jun

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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unclassified.

In (bases 1 to 10)

Matsushima, K., Haashimoto, S., Kaneko, S. and Yamashita, T.

Human liver disease-expressing genes
Human liver disease-expressing genes
Data SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)

N UP 2002209591-A/551

PF 19-JAN-2001 JP 2001012328

PF 09-JAN-2001 JP 2001012328

PF 19-JAN-2001 JP 2001012328

PF 19-JAN-2001 JP 2001012328

PF 07-2001 MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA

PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12N15/00

CC Human liver disease-expressing genes
PH Key

Location/Qualifiers

FT source

//crganism='Homo sapiens (numan)'.
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PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
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1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
Human liver disease-expressing genes
Patent: JP 2002209591-A 574 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP.
OS Home sapiens (human)
PN JP 2002209591-A/574
PP 19-JAN-2001 JP 201012328
PP 19-JAN-2001 JP 201012328
PP 19-JAN-2001 JP 201012328
PP 19-JAN-2001 JP 201012328
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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                  Indels
   Pred. No. 1.1e+02;
0; Mismatches 1;
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WED167029.

BD167029.1 GI:27872841

UP 2002209591-A/574.

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JP 2002209591-A/551.
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Best Local Similarity 88.9%;
Matches 8; Conservative (
     88.98;
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BD167006
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                                                                                  Gaps
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Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
Muman liver disease-expressing genes
Patent: JP 2002209591-Å 505 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002209591-Å/505
PD 30-JUL-2002
PP 19-JAN-2001 JP 2001012328
PP 19-JAN-2001 JP 201012328
PP KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO
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Location/Qualifiers
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C12P1/08,
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Human liver disease-expressing genes
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Key Location/Qualifiers
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Human liver disease-expressing genes.
BD166960

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JP 2002209591-A/505.
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 GI:27872681
BD166869.1 GI:27872
JP 2002209591-A/414.
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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AR301508
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AR301596/c
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Inclassified.

Inclassified.

Matchania, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human liver disease-expressing genes

Patent: JP 2002209591-A 600 30-JUL-2002,

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PP 2002209591-A/600

PP 19-JAN-2001 JP 2001012328

PI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI

YAMASHITA

PC C12P21/09,

PC C12P21/09,

PC C12P21/00,

PC C12P21/00,

PC Human liver disease-expressing genes

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Pred. No. 1.16+02;
0; Mismatches 1; Indels
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BD167055.1 GI:27872867
JP 2002209591-A/600.
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BD167237/c
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1 (bases 1 to 11)

Hebber-Katz, and methods for wound healing
Compositions and methods for wound healing
Patent: US 6538173-A 89 25-MAR-2003;
Location/Qualifiers
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Sequence 89 from patent US 6538173.
AR301508
AR301508.1 GI:31689310
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1 (bases 1 to 11)
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AUTHORS TITLE JOURNAL

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RESULT 245 AX339216/c LOCUS

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                           Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 76 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hofmann,K., Conradt,M. and Petersohn,D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 939 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
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Seguence 939 from Patent WO02053773.
AX471362
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Sequence 76 from Patent WO02053773.
AX470499 1 GI:22205624
    Mismatches

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Best Local Similarity 88.9°
Matches 8; Conservative
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AX471362
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Methods and materials to determine the p53 status of a sample by determining the binding of p53 to a vector
Patent: WO 0196602-A 10 20-DEC-2001;
MEDICAL RESEARCH COUNCIL (GB)
Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Matches 8; Conservative 0; Mismatches 1; Indels
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Heber Katz, E. Compositions and methods for wound healing Patent: US 638173-A 177 25-MAR-2003; ... Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="pGL3-Basic vector"
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/organism="Homo sapiens"
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                                                                                           /organism="unknown"
/wol_type="genomic DNA"
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Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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                                             Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02033773-A 1336 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 1415 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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               AX471759.1 GI:22206884
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Query Match 37.0%; Score 7.4; DB 1; Length 11; Best Local Similarity 88.9%; Pred. No. 1.2e+02; Matches 8; Conservative 0; Mismatches 1; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A. 997 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 617 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 617 from Patent W002053774.
AX623576.1 GI:28451517
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Sequence 997 from Patent WO02053774.
AX622956
AX623956.1 GI:28451897
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               AX624381 11 bp DNA Sequence 1422 from Patent W002053774. AX624381 GI:28452322
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Sequence 2070 from Patent W002053774.
AX625029.1 GI:28452970
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Sequence 2904 from Patent WO02053774.
AX622863 1 GI:28453901
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 10 CTGGCACGC 18
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AX624381/c
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AX625863/c
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 3587 11-JUL-2002;
Henkel Kommanditgeeellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 3587 from Patent W002053774.
AX626546 AX626546.1 GI:2845584
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Sequence 3266 from Patent WO02053774.
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AX626225.1 GI:28454263
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Matches 8; Conservative
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 5684 from Patent WO02053774.
AX628643
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Sequence 5530 from Patent WO02053774.
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Best Local Similarity 88.9%;
Matches 8; Conservative (
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 5285 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-44191 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1;
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Best Local Similarity 88.9%; Pred. No. 1.2e+02;
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Sequence 5285 from Patent W002053774.
AX628244

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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37.0%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels
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                                                             Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Petent: WO 0205374-A 6324 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 88.2.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 6947 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 7287 from Patent W002053774.

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AX630246.1 GI:28458284
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 7644 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 8038 11-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 8419 from Patent WO02053774.
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Sequence 7644 from Patent W002053774.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                              Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 8419 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Sequence 8844 from Patent WO02053774.
AX631802
AX631802.1 GI:28459909

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Matches 8; Conserv
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5 ACTCGCTGG 13
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AX456625
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AX250557/c
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BD124346.1 GI:23219291
JP 2002503460-A/117.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 11)
Katz, E.H.
                                                                                                                                                                                                                                                                                         BD124258.1 GI:23219203
DD 2002503460-A/B9.
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscate, E.H.
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Location/Qualifiers
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PN JP 2002503460-A/89
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1999 US 60/74737,26-AUG-1998 US 28-SEP-1998 US 60/102051
PC C12N15/00 Not 100 Not 
Score 7.4, DB 1, Length 11;
Pred. No. 1.2e+02,
0, Mismatches 1; Indels
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S Mus musculus (mouse)
PN JP 2002503460-A/177
PD 05-FEB-2002
                                                                                                                                                                                                                                                               Compositions and method for healing wound.
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Patent: JP 2002503460-A 89 05-FEB-2002;
THE WISTAR INSTITUTE

    .11
    /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

  37.0%;
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BD12428
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetic construct
artificial sequences.
1 (bases 1 to 9)
Hanson, A.D., Nuccio, M.L. and Henry, S.A.
S-adenosyl-1-methionine:phosphoethanolamine n-methyltransferase compositions and methods for modulating lipid biosynthesis in plants
Patent: WO 0168970-A 7 20-SEP-2001;
University of Florida (US); Carnegie-Mellon University (US)
Location/Qualifiers
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                                                                                                                                                    Compositions and method for healing wound Key
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/mol_type="genomid DNA"
/moref="taxon:32630"
/noTe="SYNTHETIC OLIGONUCLEOTIDE"
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Antisense oligonucleotides against vrl
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Sequence 97 from Patent WO0218407.
AX456625
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Sequence 7 from Patent W00168870.
AX250557
AX250557.1 GI:15984293

    .11
    /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

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Gaps

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Homo sppiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

13 1 (bases 1 to 9)

Marner(C.A., Yoo,H.W., Roberts,A.G. and Desnick,R.A. d. expression of exonic mutations in the uroporphyrinogen III synthase gene of exonic mutations in the uroporphyrinogen III synthase gene of exonic mutations in the uroporphyrinogen III synthase gene of exonic mutations in the uroporphyrinogen III synthase gene of exonic mutations in the uroporphyrinogen III synthase gene of exonic mutations in the uroporphyrinogen III synthase gene of exonic mutations in the National Library of Medicine created this general conditions from the original journal article.

This sequence comes from Figure 3.

A to G transition nt 184, Thr to Ala replacement residue 62.
                                                                                                                                                                           9 bp DNA linear PRI 07-MAY-1993
uroporphyrinogen III synthase [human, Genomic Mutant, 9 nt].
881508
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Method of detecting genetic polymorphisms using over represented
sequences
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                    Indels
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/gene="uroporphyrinogen III synthase"
Best Local Similarity 100.0%; Fred. No. 7.7e+02; Matches 7; Conservative 0; Mismatches 0;
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Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 53 from patent US 6284466.
AR167219.1 GI:16243731
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/db_xref="taxon:9606"
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1 (bases 1 to 10)
                                                              8 CGCTGGC 14
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Sattus norvegicus (Sattus Rattus norvegicus)
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Position dependent recognition of gnn nucleotide triplets by zinc
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/noEe="example target DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
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Antisense oligonucleotides against vr1
Patent: WO 0218407-A 114 07-MAR-2002;
Gruenenthal GmbH (DE)
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Patent: WO 0242459-A 2378 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
                                                                            /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Sequence 2378 from Patent W00242459.
AX668929
Patent: WO 0218407-A 97 07-MAR-2002;
Gruenenthal GmbH (DE)
Location/Qualifiers
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Sequence 114 from Patent W00218407.
AX456642
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BD238676
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C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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BD238653.1 GI:33048423
JP 2002534056-A/71.
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (hordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

(Chases 1 to 10)

Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 67 15-OCT-2002;
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60/080079 PR
60/080072 PR
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60/089853
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Location/Qualifiers
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Preparation and use of superior vaccines
Key
Location/Qualifiers
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60/09003, 19-UUN-1998 US
60/09003, 19-UUN-1998 US
60/09092, 19-UUN-1998 US
60/09000, 19-UUN-1998 US
60/09000, 19-UUN-1998 US
60/090004, 19-UUN-1998 US
60/090004, 19-UUN-1998 US
60/090001, 19-UUN-1998 US
                                                                    3D238649 10 bp DNA Preparation and use of superior vaccines.
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100.0%; Pred. No. 1.4
iive 0; Mismatches
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                          Homo sapiens (human)
JP 2002534056-A/67
15-OCT-2002
18-JUN-1999 UP 2000554749
19-JUN-1999 US 60/090039
                                                                                                     BD238649.1 GI:33048419
JP 2002534056-A/67.
                                                                                                                                             Homo sapiens (human)
Homo sapiens
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Matches 7; Conserv
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Roberts, Lo. 100

Preparation and use of superior vaccines

L. Patent, JP 200234056-A 94 15-0CT-2002,
GENZYME CORP

OS Homo sapiens (human)

PN 19 200234056-A/94

PD 15-0CT-2002

PP 18-JUN-1998 JP 2000554749

PR 19-JUN-1998 US 60/090040 PR 19-JUN-1998 US 60/090079 PR 19-JUN-1998 US 60/090079 PR
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 71 15-OCT-2002;
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60/0808079
60/080072
60/080072
60/080091
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090041,19-JUN-1998 US
090035,19-JUN-1998 US
089992,19-JUN-1998 US
089992,19-JUN-1998 US
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090048,19-JUN-1998 US
090048,19-JUN-1998 US
090078,19-JUN-1998 US
090078,19-JUN-1998 US
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60/09997.19-00N-1998 U

60/08992.19-00N-1998 U

60/08992.19-00N-1998 U

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60/08992.19-00N-1998 U

60/08004.19-00N-1998 U

60/08064.19-00N-1998 U

60/08080.19-00N-1998 U

60/08080.19-00N-1998 U

60/08099 U-19-00N-1998 U

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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
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/organism="Homo sapiens"
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JP 202534056-A/71
15-CCT-2009
18-JUN-1999 US 2000554749
19-JUN-1998 US 60/090039
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JP 2002534056-A/94.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 7; Conservative
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BRUCE L ROBER'S, SRIMIVAS SHANKARA
C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19.
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BD238708.1 GI:33048478
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 10)
Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 126 15-OCT-2002;
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60/08991 PR
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60/090048 PR
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60/090077 PR
60/090047 PR
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'organism='Homo sapiens (human)'.
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                60/090035,19-JUN-1998 US
60/08992,19-JUN-1998 US
60/08992,19-JUN-1998 US
60/08999,19-JUN-1998 US
60/08999,19-JUN-1998 US
60/080044,19-JUN-1998 US
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60/080084,19-JUN-1998 US
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60/080078,19-JUN-1998 US
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PN JP 2002534056-A/126
PF 19-CTT-2002
PF 19-UNN-1999 US 60/090041,19-UNN-1998 US 60/090035,19-UNN-1998 US 60/090035,19-UNN-1998 US 60/090035,19-UNN-1998 US 60/090035,19-UNN-1998 US 60/090035,19-UNN-1998 US 60/090004,19-UNN-1998 US 60/090004,19-UNN-1998 US 60/090004,19-UNN-1998 US 60/090004,19-UNN-1998 US 60/090044,19-UNN-1998 US 60/090076,19-UNN-1998 US 60/111715
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60/111715
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100.0%; Pred. No. 1.4
:ive 0; Mismatches
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Preparation and use of superior
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Best Local Similarity 100.
Matches 7, Conservative
     19-JUN-1998 US
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BD238708
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OS Homo sapiens (human)
PN JP 2002534056-A/518
PD 15-OCT-2002
PP 15-OCT-2002
PP 19-JUN-1999 US 60/090039,19-JUN-1998 US 60/090040 PR 19-JUN-1999 US 60/090035,19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090003 PR 19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090003 PR 19-JUN-1998 US 60/090001 PR 60/089991 PR 60/099991 PR 6
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Catarrhini; Hominidae; Homo.
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PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/56,
PC C12N1/21, C12N5/00, C12N15/00
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key
                        C12N1/19,
C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,
C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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                                             BD239100

M Preparation and use of superior vaccines. BD239100

BD239100.

JP 2002534056-A/518.

Homo sapiens (human)

M Homo sapiens (human)

M Karyota; Metazoa; Chordata; Craniata; Vert Nammala; Butheria; Primates; Catarrhini; Ho I (bases 1 to 10)

Roberts, B.L. and Shankara, S. Preparation and use of superior vaccines Patent: JP 200234056-A 518 15-OCT-2002;
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100.0%; Pred. No. 1.4
:ive 0; Mismatches
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/mol_type="genomic DNA"

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Best Local Similarity 100...
7, Conservative
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BD239100
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

RESULT 286 BD239504 LOCUS

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PAT 17-JUL-2003

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DE HOMO sapiens (human)

PN JP 2002534056-A/944

PD 15-0CT-2002

PF 18-UTN-1999 UP 2000554749

PR 19-UTN-1998 US 60/090031,19-UTN-1998 US 60/090079

PR 19-UTN-1998 US 60/090035,19-UTN-1998 US 60/090079

PR 19-UTN-1998 US 60/080992,19-UTN-1998 US 60/090079

PR 19-UTN-1998 US 60/080992,19-UTN-1998 US 60/080993 PR 60/080992,19-UTN-1998 US 60/080993 PR 60/080901 PR 60/080992,19-UTN-1998 US 60/080993 PR 60/0809001,19-UTN-1998 US 60/080993 PR 60/080992,19-UTN-1998 US 60/080993 PR 60/080992,19-UTN-1998 US 60/08094 PR 60/080994,19-UTN-1998 US 60/090044 PR 60/090044,19-UTN-1998 US 60/090043 PR 60/090044,19-UTN-1998 US 60/090047 PR 60/090944,19-UTN-1998 US 60/090047 PR 60/090078,19-UTN-1998 US 60/0900
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[ (bases 1 to 10)

Roberts, B. L. and Shankara, S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 985 15-OCT-2002;
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                                   linear
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Treparation and use of superior vaccines. BD239526 BD239526.1 GI:33049296
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JP 2002534056-A/985.
Homo sapiens (human)
Homo sapiens
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PC __CLANIS/00,C12NS/00,C12N15/00
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UP 2002534056-A/922.
UP 2002534056-A/922.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutberia; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 10)
Roberts; B.L. and Shankara; S.
Preparation and use of superior vaccines
Patent: JP 200254056-A 922 15-OCT-2002;
GENZYME CORP
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OS UNCESSAGES (human)

PN UP 2002534056-A/922

PD 15-CCT-2002

PF 18-CUN-1999 UP 2000554749

PR 19-UNN-1998 US 60/090041,19-UNN-1998 US 19-UNN-1998 US 60/080997,19-UNN-1998 US 19-UNN-1998 US 19-UNN-1998 US 60/080992,19-UNN-1998 US 19-UNN-1998 US 60/080991,19-UNN-1998 US 19-UNN-1998 US 60/08041,19-UNN-1998 US 19-UNN-1998 US 60/08044,19-UNN-1998 US 19-UNN-1998 US 60/08060,19-UNN-1998 US 19-UNN-1998 US 60/08080,19-UNN-1998 US 19-UNN-1998 US 60/08080,19-UNN-1998 US 19-UNN-1998 US 60/08080,19-UNN-1998 US 19-UNN-1998 US 60/08080,19-UNN-1998 US 19-UNN-1998 US 60/08076,19-UNN-1998 US 19-UNN-1998 US 19-UNN-1
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0;
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                                              /db_xref="taxon:9606"
                                                                                                   Query Match
Best Local Similarity 100.
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GENZYME CORP
OS Home sapiens (human)
PN 19202334056-A/985
PN 15-0CT-2002
PF 18-JUN-1999 US 60/090040 PR 19-JUN-1998 US 60/090040 PR 19-JUN-1998 US 60/090079 PR 19-JUN-1998 US 60/090077 PR 60/090070 PR 19-JUN-1998 US 60/090077 PR 60/090077 PR 19-JUN-1998 US 60/090077 PR 60/09007 PR
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N Preparation and use of superior vaccines.
BD239630.
BD239630.1 GI:33049400

JP 2002534056-AA/1048.
HOMO sapiens (human)

M HOMO sapiens (human)

M HOMO sapiens (human)

Rukaryota; Metazoa; Chordata; Craniata; Ver'

Mammalia; Eutheria; Primates; Catarrhini; H

1 (bases 1 to 10)

Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1048 15-OCT-2002;
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BD239630
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60/08004.19-JUN-1998 US
60/08004.19-JUN-1998 US
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TON BD240040.

BD240040.

BD240040.1 GI:33049810

BD240040.1 GI:33049810

BD2400534056-A/1458.

Homo sapiens

BUARAZOA, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates; Catarrhini; Hominidae; Homo.

RS Roberts, BL. and Shankara, S.

Preparation and use of superior vaccines

N. Patent: JP 2002534056-A 1458 15-OCT-2002;

GENTALE CORP.

C. 1 (2002) A 1458 15-OCT-2002;
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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/09004,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089094,19-JUN-1998 US 60/0890077 PR
19-JUN-1998 US 60/089076,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PT REUCE L ROBERTS, SRINIYAS, SHANKARA
PC CL2N15/09,7C12N15/09,AG1K39/00,AG1P35/00,AG1P37/04,C12N1/15,
C12N1/19,
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Location/Qualifiers
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PN JP 2002534056-A/1458

PP 15-OT-2002

PF 18-JUN-1998 US 60/089997, 19-UU

19-JUN-1998 US 60/089997, 19-UU

19-JUN-1998 US 60/089997, 19-UU

19-JUN-1998 US 60/089997, 19-UU

19-JUN-1998 US 60/089999, 19-UU

19-JUN-1998 US 60/089999, 19-UU

19-JUN-1998 US 60/089999, 19-UU

19-JUN-1998 US 60/080040, 19-UU

19-JUN-1998 US 60/08004, 19-UU

19-JUN-1998 US 60/08004, 19-UU

19-JUN-1998 US 60/08099, 19-UU

19-JUN-1998 US 60/08099, 19-UU

19-JUN-1998 US 60/08099, 19-UU

19-JUN-1998 US 60/08099, 19-UU
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PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC G01N37/00,
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(bases 1 to 10)

Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1968 15-OCT-2002;
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Location/Qualifiers
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35.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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Preparation and use of superior vaccines
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Preparation and use of superior vaccines
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60/090035,19-UUN-1998 US
60/090035,19-UUN-1998 US
60/090035,19-UUN-1998 US
60/090000,19-UUN-1998 US
60/090000,19-UUN-1998 US
60/090042,19-UUN-1998 US
60/090044,19-UUN-1998 US
60/090081,19-UUN-1998 US
60/090081,19-UUN-1998 US
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60/090081,19-UUN-1998 US
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    /organism="Homo sapiens"
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JP 202534056-A/1968
15-OCT-2002
18-JUN-1999 US 60/090039
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BD240550
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TITLE
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1 (bases 1 to 10)
Hashimoto, S., Matsushima, K. and Suzuki, T.
Genes with human dendritic cell expression
Patent: JP 2000279181-A 276 10-OCT-2000;
SCIENCE & TECH AGENCY
OS Homo saplens (human)
PN JP 2000279181-A/276
PD 10-OCT-2000
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  linear
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  B39743 10 bp DNA 1
Genes with human dendritic cell expression.
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Polyak,K., Vogelstein,B. and Kinzler,K.W. P53-induced apoptosis
Patent: US 6432640-A 41 113-AUG-2002;
Location/Qualifiers
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AR222988 11 GI:23330826
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                                    E39743.
E39743.1 GI:18621834
JP 2000279181-A/276.
Homo sapiens (human)
Homo sapiens
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PAT 01-MAY-2001

linear

RESULT 294 AR241894/c LOCUS

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL FEATURES

ORGANISM

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Memo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0127267-A 10 19-APR-2001;
ISIS INNOVATION LIMITED (GB)
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Patent: WO 0100849-A 130 04-JAN-2001;
ICOS CORPORATION (US)
Location/Qualifiers
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Patent: WO 0138577-A 29 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 29 from Patent WO0138577.
AX152114
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Equence 10 from Patent W00127267.
AX112963
AX112963.1 GI:13939398
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Tankyrase2 materials and methods
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Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 182 29-OCT-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.

1 (bases 1 to 10)
Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
Androgen-regulated gene expressed in prostate tissue
Patent: Uccation/Qualifiers
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AR241894
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AX152532.1 GI:14534183
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                                       Homo sapiens (human)
Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0138577-A 237 31-MAY-2001;
The John Hopkins University (US)
Location/Qualifiers
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Patent: WO 0138577-A 289 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 237 from Patent WO0138577.
AX152322 AX152322.1 GI:14533973

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    .10
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0138577-A 455 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Patent: WO 0138577-A 665 31-MAY-2001;
                                                                    Velculescu, V.E., Vogelstein, B. and Kinzler, K.W. Human transcriptomes
Patent: WO 0138577-447 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Sequence 455 from Patent WO0138577.
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Sequence 665 from Patent WO0138577.
AX152750
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PAT 22-JUN-2001

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0138577-A 1146 31-MAY-2001;
The Johns Hopkins University (US)
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Sequence 1146 from Patent WO0138577.
AX153231.1 GI:14534882
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Sequence 59 from Patent WO0210454.
AX374638 AX374638.1 GI:19169535
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Squence 98 from Patent WO0175177.
AX302580. GI:17383107
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catàrrhini; Hominidae; Homo.
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                                                                                                                      Query Match 35.0%; Score 7; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Human transcriptomes
Patent: WO 0138577-A 873 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Patent: WO 0138577-A 951 31-WAY-2001,
The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      DNA
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Sequence 951 from Patent WO0138577.
AX153036
                               1. 10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                    10 bp 1
Sequence 873 from Patent W00138577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
The Johns Hopkins University (US)
Location/Qualifiers
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Homo sapiens
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Homo sapiens
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AX152958
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AX153036
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PAT 30-NOV-2001

PAT 01-MAR-2002

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SOURCE ORGANISM

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TITLE JOURNAL REFERENCE AUTHORS

FEATURES

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BD008019.

BD008019.

JP 200106993-A/295.

Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (hordata, Craniata, Vertebrata, Euteleostomi, Euterrycta, Metazoa, Chordata, Craniata, Vertebrata, Homo.

En (bases 1 to 10)

SM Homo sapiens (human monocyte expressing genes

LPS activated human monocyte expressing genes

LPATONIC SM HOMO SAPIENS (human)

NO SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 200106999-A/295

PD 21-MAR-2001

PR 28-APR-2000 JP 2000131079

PR PR 28-APR-2000 JP 2000131079
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DP JP 201069993-A/255
PD 21-MAR-2001
PP 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA.SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
CC A61P31/00,C12P21/08,C12N15/00
CC LCCation/Qualifiers
FH Key L.10
PT SOURCE (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rce 1. .10 /organism='Homo sapiens (human)'. Location/Qualifiers
                                                                                                                                                                                                                                 ce 1. .10
/organism='Homo sapiens (human)'.
Location/Qualifiers
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.larity 100.0%; Pred. No. 1.46+02;
Conservative 0; Mismatches 0; Indels
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0, 1.4e+02;
ches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.4
Matches 7; Conservative 0; Mismatches

    .10
    /organism="Homo sapiens"
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/organism="Homo sapiens"
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Best Local Similarity
Matches 7; Conserv
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1 (bases 1 to 10)

Matsubhima, K., Hashimoto, S. and Suzuki, T.

IPS activated human moncyte expressing genes
Patent: JP 2001069993-A 255 21-MAR-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hustert, E., Haberl, M. and Wojnowski, L.
Identification of the genetic determinants of the polymorphic cyp3as expression
Patent: WO 0205375-A 81 11-JUL-2002;
EPIDAUROS BIOTECHNOLOGIE AG (DE)
Location/Qualifiers
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BD007979
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     Ouery Match 35.0%; Score 7; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                Choi, J.Y., Koshy, B., Kliem, S. and Stephens, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                      Haplotypes of the alas2 gene
Patent: WO 0210454-A > 59 07-FEB-2002;
Genaissance Pharmaceuticals, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .10
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Seguence 81 from Patent WO02053775.
AX472090
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UP 2001069993-A/255.
Homo sapiens (human)
Homo sapiens
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Homo sapiens
                            Homo sapiens (human)
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                                                     Homo sapiens
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RESULT 309
AX472090
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KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

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PAT 31-JAN-2002

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REFERENCE AUTHORS TITLE JOURNAL

RESULT 310 BD007979 LOCUS

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REFERENCE AUTHORS TITLE JOURNAL

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Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0;
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PN JP 20
PD 30-JU
PF 19-JA
PI KOJI |
YAMASHITA
PC C12N1|
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

B 1 (bases 1 to 10)

S 200163241-A 41 27-NOV-2001;

THE OCHENT UP 20015341-A 41 27-NOV-2001;

THE OCHEN HOPKINS UNIVERSITY
OS Home sapiens (human)
PN 7P 20153341-A 41
PP 17-SEP-1998 JP 2000511894
PR 17-SEP-1999 JP 2000511894
PR 17-SEP-1997 US 60/059153,30-MAR-1998 US 60/079817 PI
BERT VOGELGTEIN, KENNETH W KINZLER, KORNELIA POLYAK PC
C12Q1/68,COTK16/32,C12P21/08/C12N15/09,C12N15/00 CC P53-induced
apoptosis

Location/Qualifiers
FH Key L. 10
PT SOURCE L.
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                                     PAT 27-AUG-2002
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BD143088.1

Synthetic construct

Synthetic construct

Synthetic construct

artificial sequences.

E 1 (bases 1 to 10)

Synthetic construct

B 1 (bases 1 to 10)

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                                     linear
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                     DNA
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                     10 bp
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JP 2001523441-A/41.
Homo sapiens (human)
Homo sapiens
                                 BD091163
P53-induced apoptosis.
BD091163
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

FEATURES

REFERENCE

RESULT 313 BD143088 LOCUS

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PAT 17-JAN-2003
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Human liver disease-expressing genes.

Hol66515.1 G1:27872327

D10 2002209591-A/60.

Unidentified

Unid
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ON Human liver disease-expressing genes.
NA BD166632.1
BD169209591-A/177.
BM1081 liver disease-expressing genes
BM2081 liver disease-expressing genes
BM208209591-A/177 30-JUL-2002;
BM2081 liver disease-expressing genes
BM208209591-A/177
BM208209
Gaps
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/organism='Homo sapiens (human)'.
Location/Qualifiers
        Indels
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Key Location/Qualifiers
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rge

source

q

FEATURES

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Query Match 35.0%; Score 7; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   1..10
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/db_xref="taxon:32630"

    .12
    /organism="Homo sapiens"
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JP 2002517434-A/81.
Homo sapiens (human)
Homo sapiens
        synthetic construct artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 GCACGCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 318
BD234977/c
LOCUS
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TITLE
JOURNAL
          ORGANISM
                                       REFERENCE
AUTHORS
TITLE
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                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unclassified.

1 (bases 1 to 10)

Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.

Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.

Matsushima, E. 2002209591-A 269 30-UUL-2002;

Japan SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)

PD 30-UUL-2002

PD 30-UUL-2002

PF 19-JAN-2001 JP 2001012328

PI 19-JAN-2001 JP 2001012328
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                                                                                    /organism='Homo sapiens (human)'. Location/Qualifiers
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                                                                                                                                                                                                     Query Match 35.0%; Score 7; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.0%; Score 7; DB 1; Length 10; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
C12P21/08,
C12N1S/00
Human liver disease-expressing genes
Location/Qualifies
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Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           N Human liver disease-expressing genes.
1 BD166724
BD166724.1 GI:27872536
Up 2002209591-A/269.
unidentified
unidentified
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/db_xref="taxon:32644"

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    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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BD168603.1 GI:27874415
WO 0230440-A/4.
synthetic construct
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Matches 7; Conservative
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C12N15/00
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                                                                                                                                                                                                                                                                     11 TGGCACG 17
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PC C12N1
PC C12P2
PC C12N1
CC Human
FH Key
FT SOULC
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          FEECE
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BD166724/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ONGANISM
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BD168603/c
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TITLE JOURNAL REFERENCE AUTHORS

COMMENT

FEATURES

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PAT 17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Challingensiepen, K.H., Schlingensiepen, R. and Brysch, W. and the for trimulating the immune system.

Amethod for trimulating the immune system.

Parent: JP 2002517434-A 81 18-JUN-2002;

BIOGNOSTIX GESELLSCHAFF FUER BIOMOLEKULARE DIAGNOSTIK MEH SO HOMO explens (human)

PD 200251744-A/81.

PD 18-JUN-2002 JP 2000553044

PP 10-JUN-1998 EP 98110709.7, 25-JUL-1998 EP 98113974.4 PI

KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395

PC 00,A61P35/02,61P37/02,C12N15/09,A61K37/02,C12N15/00 CC

Method for stimulating the immune system

EH Key

1.12

FT source

/organism='Homo sapiens (numan)'

/organism='Homo sapiens (numan)'
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                                                                                                                                                                                                                                                                                                                          /organism='Artificial Sequence'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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A method for stimulating the immune system.
BD234977
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LOCUS

ACCESSION VERSION KEYWORDS SOURCE

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' Tue Jun 8 12:32:41 2004

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4 GACTCGC 10 ||||||| 7 GACTCGC 1

Search completed: June 8, 2004, 12:21:51 Job time: 1 secs